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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                   ĕ
                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                   Score
                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
    922992292
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                                                                                                                                                                 Match
                            1000
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11:
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92
                                                                                                                                                                                                                                                                                   /SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May 23, 2001, 16:14:49; Search time 18.65 Seconds (without alignments) 45.976 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390729 seqs, 57163235 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS6/gcgdata/geneseq/geneseqp/AA1984.DAT:*
                                                                                                                                                                 Length
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 R12973
R83639
R81292
W011392
W56114
Y04481
Y04481
Y78574
W46044
W13025
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Human type IV coll
Type IV collagen d
Collagen sequence
Collagen alphal(IV
Peptide intermedia
                                                               IV-H1 based on typ
Collagen IV alpha-
Non-RGD, non-YISGR
Peptide 10 for gli
Collagen alphal(IV
Peptide representi
                                                                                                                                                                Description
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R12973
ID R1
    XPXPXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                malignant cell growth; melanoma cell motility; cellular adhesion.
                                                                                                                                                                                                                                                                                                                                                                      24-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                 R12973;
                                                                                                                                                                                                                                                                                                                                                                                                                         R12973 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                        IV-H1 based on type IV collagen alpha 1 chain triple helical region
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ALIGNMENTS

(first entry)

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Polypeptide for promoting tumour cell adhesion, spreading and motility - useful in chemo:diagnosis and chemotherapy of malignant cell growth Claim 1; Page 26; 37pp; English. Chelberg MK, Tsilibary PE, McCarthy JB; WPI; 1991-207864/28. 14-DEC-1989; 06-DEC-1990; 27-JUN-1991 W09108755-A (MINU) MINNESOTA UNIVERSITY 89US-0450419. 90WO-US07162.

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Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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                                                                                                                                 Sequence
                                                                                                                                                                                                        fibroblast, epithelial and glial cell proliferation, contraction of epiretinal membranes and cell migration within the eye. It may be used in the treatment of proliferative vitreoretinopathy,
                                                                                                                                                                                                                                                                                        A polypeptide which includes at least five amino acids from a fragment of the fibronectin A chain (R83679-84), C-terminal G domain of the laminin A chain (R83642/78) or NCl domain of the alpha-2 chain of type IV collagen (R83639-41) suppresses
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 29; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-320291/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agarwal A,
Wright MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09522979-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proliferation; suppression; epithelial; membranes; contraction; migration; vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen IV alpha-2 chain NC1 domain peptide IV-H1 (1263-1277).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen
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28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vitreoretinal; glaucoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R83639 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gvkgdkgnpgwpgap 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferative vitreo:retinopathy, retinal scarring
- using peptide derived from fibronectin, laminin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type IV; alpha-2 chain; NC1 domain; fibroblast; cell;
tion; suppression; epithelial; glial; epiretinal; eye;
contraction; migration; vitreoretinopathy; scarring;
                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Balles M, Furcht LT, Skubitz AP;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                 AA;
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94US-0203458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
                     100.0%;
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                                                                                                                                                                                  and glaucoma
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0;
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                     Score 92; DB 16;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 12;
Pred. No. 2.6e-07;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DS,
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                                                 Length
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or
0,
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Indels

Gaps

Synthetic

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RESULT
W01139
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R82922
ID R8
XX
AC R8
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Вþ
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                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                      The peptides R70472-90 and R82907-24 are peptide derivatives which inhibit cancer metastasis. They are composed of an adhesive peptide with a core sequence selected from: RGD (R70472-85), YIGSR (R70486-90) or other sequence (R82907-24), linked to a water soluble polysaccharide, preferably a water soluble dextran, at the C-terminus. The peptides are useful in inhibiting cancer metastasis, healing wounds and the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer metastasis inhibitive peptide derivs. - useful for of cancer metastasis, healing of wounds and regulation of
                                               glia cell; neuron; analysis; behaviour; selective; removal
                                                                         Peptide 10
                                                                                                   18-DEC-1996
                                                                                                                            W01139;
                                                                                                                                                    W01139 standard;
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                           of immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3; 6pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer metastasis; adhesive peptide; core sequence; water soluble polysaccharide; metastasis; wound; im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R82922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JAPG ) NIPPON ZEON KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP07089999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-RGD, non-YISGR cancer metastasis inhibitory peptide #16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R82922 standard;
                                     Laminin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenicity.
                                                                                                                                                                                                                                                                      Local Similarity hes 15; Conser
                                                                                                                                                                                                                                            1 GVKGDKGNPGWPGAP 15
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                                                                                                                                                                                                                    gvkgdkgnpgwpgap
                                     fibronectin;
                                                                         for glia cell removal derived
                                                                                                                                                                                                                                                                                                                                   15 AA;
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polysaccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-0254779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93JP-0254779
                                                                                                                                                   peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide; 15
                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                     collagen.
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                                                                                                                                                                                                                                                                     Score 92; DB 16;
Pred. No. 2.6e-07;
; Mismatches 0;
                                                                          from collagen
                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogenicity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibition
                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                      Gaps
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RESULT
W13022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
Solid phase synthesis of triple-helical branched polypeptide under O-glycosidic bond and deuterium label retaining conditi which may contain collagen cell adhesion sequences, useful fo studying structure and biological activity of collagen
                                                                                                                                                                                                                                           Collagen; cell; adhesion; migration; promotion; alphal(IV) chain; triple helical polypeptide; solid phase synthesis; study; O-glycosidic bond; deuterium label; structure; biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W01135-40 are peptides, derived from laminin, fibronectin and collagen, which selectively remove glia cells in the presence of neurons. This enables analysis of behaviour of neurons in the absence of glia cells.
                                                                                                                                                                                                                                                                                                                                  W13022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selective remover for glia cells from neuronal cell cultures - useful for studying behaviour of neurons in the absence of glia
                                                       WPI; 1997-011309/01
                                                                             Fields
                                                                                                                      30-JUN-1993;
27-SEP-1995;
                                                                                                                                                                                                  US5576419-A
                                                                                                                                                                                                                                                                                       Collagen alpha1(IV)
                                                                                                                                                                                                                                                                                                             30-APR-1997
                                                                                                                                                                                                                                                                                                                                                      W13022 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP08073495-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                  (MINU ) UNIV
                                                                                                                                                        30-JUN-1993;
                                                                                                                                                                             19-NOV-1996
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 4; 6pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEN ) AGENCY OF IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                      GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                          gvkgdkgnpgwpgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                   MINNESOTA
                                                                                                                      93US-0085633
95US-0534342
                                                                                                                                                       9308-0085633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94JP-0232263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0232263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Pro-NH2"
                                                                                                                                                                                                                                                                                       chain residues 1263-1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; DB 17;
2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                     conditions,
             for
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                 sequence. This sequence is used to construct a peptide-amphiphile complex to exemplify the invention. The peptide-amphiphile complex of the specification comprises a lipophilic portion and a peptide portion having a secondary structure. The peptide portion preferably has biological activity, e.g. cell recognition activity or enzymatic activity. The complex may be used for forming stable lipid films on substrates, or may be used in bilayer membrane systems. It may, in micellar or vesicular form, be used in preparation of drug-targeting systems are the form.
                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present peptide is a collagen cell adhesion sequence (CCAS), known to promote adhesion and migration of various cells, comprising residues 1263-1277 of the collagen alphal(IV) chain. The triple helical polypeptide 2 (THP-2), which includes the present CCAS (residues 25-39) in its triple helix inducing region, was prepared by solid phase synthesis under O-glycosidic bond and deuterium label retaining conditions. THP-2 can be used to study
                                                                                                                                                                                          Claim 15;
                                                                                                                                                                                                                                    Peptide-amphiphile complexes which are able to form micelles or vesicles - comprise a lipophilic portion and a peptide portion or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alpha-1(IV)1263-1277 collagen sequence; peptide-amphiphile complex; lipophilic portion; stable lipid film; bilayer membrane system;
                           systems against melanoma cells.
                                                                                                                                                             The present sequence represents the alpha-1(IV)1263-1277 collagen
                                                                                                                                                                                                                                                                                                              Fields GB,
                                                                                                                                                                                                                                                                                                                                                                         23-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09807752-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug-targeting; melanoma cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide representing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W56114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W56114 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                          (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the structure and biological activity of collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                  1998-179051/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                        secondary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                          Page 23; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AA;
                                                                                                                                                                                                                                                                                                              Tirrell MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                       96US-0702254.
                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US14145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the alpha-1(IV)1263-1277 collagen sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                    portion which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Sequence

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Y04481
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                                                  Best Local Similarity Matches 15; Conserv
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative (
                                                                                                                               The present sequence represents an all D-form fragment of the continuous collagenous region of the major triple helical domain of the alpha 1 chain of human type IV collagen, designated D-IVHI. The peptide D-IVHI can be used to inhibit tumour cell binding to type IV collagen, inhibit tumour cell invasion of basement membrane and inhibit tumour cell metastasis in vivo. The peptide can be used to treat melanoma cell metastasis, and spontaneous Lewis lung tumour metastasis. The peptide is also useful for targeting cytotoxic agents and drugs to tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell
                                                                                                             Sequence
                                                                                                                                                                                                                                           Claim 4; Page 18; 31pp; English
                                                                                                                                                                                                                                                                   New polypeptide useful for inhibition of tumour cell adhesion to IV collagen
                                                                                                                                                                                                                                                                                                        WPI; 1999-302644/25
                                                                                                                                                                                                                                                                                                                             Fields GB, McCarthy JB
                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9920300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human type IV collagen alpha 1 chain D form fragment D-IVH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y04481;
                                                                                                                                                                                                                                                                                                                                                     (MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                            22-OCT-1997;
22-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y04481 standard; peptide; 15
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1 gvkgdkgnpgwpgap
               1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gvkgdkgnpgwpgap
                                                                                                             15 AA;
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 1 chain; D-IVH1; inhibition; tumour; major triple helical domain; collagenous region.
                                                                                                                                                                                                                                                                                                                                                                            97US-0062716.
97US-0062617.
                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US22405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-form residues"
                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ
                                                             Score 92; DB 20;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 19;
Pred. No. 2.6e-07;
; Mismatches 0;
                                                  Mismatches
                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                          15;
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                Gaps
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RESULT Y78574

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RESULT
W46044
ID W4
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                                                                                                                                                                                                                                                                                                                                                       XX PX XX OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a type IV collagen peptide. Ocular administration of the peptide inhibits fibroblast proliferation and can be used in the treatment of glaucoma. The peptide can be used to treat proliferative vitreoretinopathy by ocular administration of the peptides of the invention, which suppress fibroblast-mediated collagen gel contraction. The peptides can be used for treating glaucoma in mammals, especially humans, by inhibiting intraocular fibroblast proliferation, fibroblast migration and scarring.
                                  Modified-site
                                                                     Synthetic
                                                                                           Triple helix;
                                                                                                                 Collagen sequence synthesised as triple-helical peptide
                                                                                                                                          23-DEC-1998
                                                                                                                                                                 W46044;
                                                                                                                                                                                      W46044 standard;
                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of glaucoma by ocular administration of a peptide that inhibits fibroblast proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gregerson DS, Agarwal A, Furcht LT, Balles M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type IV collagen; proliferative ret:
            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-159882/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y78574 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                            Local Similarity 100 es 15; Conservative
                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                          1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                              ٥
                                                                                                                                                                                                                                               gvkgdkgnpgwpgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IV collagen derived peptide IV-HI
                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Column
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                           collagen structure;
                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gen; intraocular fibroblast proliferation inhibitor;
retinopathy; fibroblast migration; scarring; glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0203458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0394748
/label= 4Hyp
                                             Location/Qualifiers
                       /label= 4Hyp
                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wright MM,
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                       Score 92; DB 21;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                            homo-trimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murali S,
                                                                                            hetero-trimer
                                                                                                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skubitz APN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type IV collagen
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                             Gaps
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В
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Best Local S
Matches 15
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27-SEP-1995;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to supported polypeptides of formula:
A-B-B-(J)j-(U)u-L-R; where A = an Nalpha-amino protecting group
removable under non-acidic conditions; B = an amino acid having a single
side-chain amino group protected with a group removable under non-strong
acidic conditions; J = an amino acid that is capable of acting as a
chromophore and is protected with a group capable of withstanding the
conditions under which the protecting groups of A and B are removed; U =
an amino acid; u = 0 or 1; j = 1 or more; L = a linker capable of being
labilised using a non-strong acid mechanism, and R = a support material.
The supported polypeptides are intermediates for triple-helical
polypeptides. The triple-helical polypeptides are useful for studying the
structure and biological activity of specific collagen sequences in homo-
                                                                                                          Triple helical polypeptide; collagen; cell; adhesion; migration; promotion; alphal(IV) chain; solid phase synthesis; study; O-glycosidic bond; deuterium label; structure; biological activity; homotrimeric; heterotrimeric; nuclear magnetic resonance; NMR.
                                                                                                                                                                                                                                       W13025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Supported polypeptide(s) useful as intermediates - for triple-helical polypeptide(s) having collagen structures
             Modified-site
                                                                                                                                                                               Collagen alphal(IV) chain containing triple helical polypeptide 4.
                                                                                                                                                                                                          30-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-192815/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                               W13025 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-1996;
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                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                               1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hetero-trimeric forms. The present sequence represents a collagen uence used in the synthesis of triple-helical peptides.
                                                                                                                                                                                                                                                                                                                                   gvkgdkgnpgwpgap
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Column 3;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MINNESOTA
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95US-0534342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0675140
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∕label- 4Hyp
             σ
                                          Location/Qualifiers
/label- Hyp
                          /label- Hyp
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                      Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT
W46046
ID W46
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Best Local
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                                                                                                   W46046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Solid phase synthesis of triple-helical branched polypeptide - under O-glycosidic bond and deuterium label retaining conditions, which may contain collagen cell adhesion sequences, useful for studying structure and biological activity of collagen
                                        Peptide intermediate used in synthesis of triple-helical peptide
                                                                      23-DEC-1998
                                                                                                                              W46046 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                       overlapping NMR resonances.
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27-SEP-1995;
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95US-0534342.
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Pred. No. 4.8e-07;
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Triple helix; collagen structure; homo-trimer; hetero-trimer

Synthetic

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Best Local Similarity
Matches 15; Conserv
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27-SEP-1995;
03-JUL-1996;
                                                                                                                  The invention relates to supported polypeptides of formula:
A-B-B-(J)j-(U)u-L-R; where A = an N alpha-amino protecting group
removable under non-acidic conditions; B = an amino acid having a single
side-chain amino group protected with a group removable under non-strong
acidic conditions; J = an amino acid that is capable of acting as a
chromophore and is protected with a group capable of withstanding the
conditions under which the protecting groups of A and B are removed; U =
an amino acid; u = 0 or 1; J = 1 or more; L = a linker capable of being
labilised using a non-strong acid mechanism, and R = a support material.
The supported polypeptides are intermediates for triple-helical
polypeptides. The triple-helical polypeptides are useful for studying the
structure and biological activity of specific collagen sequences in homo-
and hetero-trimeric forms. The present sequence represents a peptide
intermediate used in the synthesis of a triple-helical peptide.
                                                                                                Sequence
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Modified-site
1 GVKGDKGNPGWPGAP 15
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                                      Conservative
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95US-0534342.
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                                    0;
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                                                Score 92; DB 19;
Pred. No. 7.1e-07;
                                    Mismatches
                                                          Length 39;
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RESULT 12
W46043
ID W46043
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AC W46043
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DT 23-DEC
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                     The invention relates to supported polypeptides of formula:

A-B-B-(J))-(J)u-L-R; where A = an N alpha-amino protecting group

removable under non-acidic conditions; B = an amino acid having a single

side-chain amino group protected with a group removable under non-strong

acidic conditions; J = an amino acid that is capable of acting as a

chromophore and is protected with a group capable of acting as a

conditions under which the protecting groups of A and B are removed; U =

an amino acid; u = 0 or 1; j = 1 or more; L = a linker capable of being

labilised using a non-strong acid mechanism, and R = a support material.

The supported polypeptides are intermediates for triple-helical

polypeptides. The triple-helical polypeptides are useful for studying the

structure and biological activity of specific collagen sequences in homo-

and hetero-trimeric forms. The present sequence represents a collagen

sequence used in the synthesis of triple-helical peptides.
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27-SEP-1995;
03-JUL-1996;
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                                                                                                                                                                                                                                                                          Supported polypeptide(s) useful as intermediates - for triple-helical polypeptide(s) having collagen structures
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Solld phase synthesis of triple-helical branched polypeptide - under O-glycosidic bond and deuterium label retaining conditions.
                          WPI; 1997-011309/01
                                                                           30-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Triple helical polypeptide; collagen; cell; adhesion; migration; promotion; alphal(IV) chain; solid phase synthesis; study; O-glycosidic bond, deuterium label; structure; biological activi: homotrimeric; heterotrimeric; nuclear magnetic resonance; NMR.
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comprising
sequence"
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Pred. No.
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Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antipacterial; diagnosis; neural disorder; immune disorder; reproductive;
                                                          Claim 11; Page 996-998; 1425pp; English.
                                                                                    Lung cancer associated gene sequences, referred antigens, useful for treatment, prevention, and such as lung cancer -
                                                                                                                                                 WPI; 2000-587514/55
N-PSDB; F18045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 gvkgdkgnpgwpgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                 SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                        2000WO-US05918
                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
                                                                                                                                                                                                                                                                          99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                               wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                               healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                     to as lung cancer
diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Polynucleotide sequences F17982 - F18424 encode human lung cancer associated proteins represented in B58106 - B58548. Lung cancer associated proteins and polynucleotide sequences, their agonists,

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RESULT 15
R23873
ID 723873
XX R23873
XX R23873
XX R23873
XX Mutati
XX Mutati
XX Mutati
XX Musc-d
FT Misc-d
FT ISolat
PT Isolat
PT Lisolat
PT Liso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointsstinal general; nephrotropic; antlinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neutral impure markers.
                           Isolation of DNA encoding alpha-5(IV)polypeptide of type collagen - to detect mutations in genes for alpha-5(IV) c which produce genetic or acquired basement membrane disore.g. Alport's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences F18425 - F18433 and peptide B58549 are used in the course of the invention for the identification and characterisation.
                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "
Misc-difference 275..277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "interruption in Gly-X-Y sequence"
Misc-difference 159..160
                                                                                                                                                                         WPI; 1992-192174/23
N-PSDB; Q24551.
                                                                                                                                                                                                                                                             Hostikka SL,
                                                                                                                                                                                                                                                                                                                      (TRYG/) TRYGGVASON K.
                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5114840-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutations; Alport's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha 5 (IV) of type IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R23873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R23873 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the polynucleotide and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKGDKGNPGWPGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                          Tryggvason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                             89US-0377238
                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0377238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 43..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456..458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "interruption"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "interruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "interruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "interruption in Gly-X-Y sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              basement membranes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in Gly-X-Y sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in Gly-x-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; I
. 6.3e-05;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gly-x-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                         (IV) chain disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 16
W09643
ID W09643
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Best Local Similarity
                                                                                     20-DEC-1990;
07-JUL-1989;
11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type IV collagen, the major component of basement membranes. The protien contains the Gly-X-Y repeat coding sequence typical for collagenous proteins at one end and a typical NC-domain coding sequence at the other end. The sequence can be used to detect mutations in individual genes specific for this chain which can, directly or indirectly, produce several human diseases. It can also be used to determine genetic, e.g. Alport's syndrome, or acquired e.g. diabetes mellitus, disorders of the basement membrane, acquired e.g. diabetes mellitus, disorders of the basement membrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen alpha5(IV); basement membrane; Alport's syndrome;
nephritis; kidney; renal failure; antibody; diagnosis; COL4A5 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and as probes or antibodies against these nucleotide sequences. Gene fragments generated through amplifications from human genomic or cloned DNA can also be used for detection and analysis of genes.
 Hostikka
                                         (HOST/) HOSTIKKA S L. (HOYH/) HOYHTYA M.
                                                                                                                                               07-JUL-1989;
                                                                                                                                                                             14-JAN-1997.
                                                                                                                                                                                                          US5593900-A
                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human type IV collagen alpha-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09643 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                             (TRYG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1997
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366 gikgekgnpgqpglp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is that of the alpha 5(IV) polypeptide chain of human _2 IV collagen, the major component of basement membranes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
 SL,
                             TRYGGVASON K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Hoyhtya
                                                                                     89US-0377238
94US-0321084
                                                                                                                  90US-0630563
                                                                                                                                               89US-0377238
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                                                                                                                                                                                                                                                                                                                           /label= Collagenous_domain
/note= "collagenous domain contains Gly-X-Y
/note= "ripeptide repeats, interrupted at
positions 43-47, 159-160, 275-276,
456-459"
                                                                                                                                                                                                                                                                                   742..751
                                                                                                                                                                                                                                                                                              544 772
/label= Non-collagenous_domain
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..543
                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                    /label= Immunogenic_peptide
/note= "peptide used to rai:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%;
73.3%;
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 Z
                                                                                                                                                                                                                                    peptide used to raise diagnostic antibodies (Claim 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                772
Tryggvason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; D
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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0.037;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                           Triple helical polypeptide; collagen; cell; adhesion; migr promotion; alphal(IV) chain; solid phase synthesis; study; O-glycosidde bond; deuterium label; structure; blological homotrimeric; heterotrimeric; nuclear magnetic resonance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W13024;
Solid phase synthesis of triple-helical branched polypeptide - under O-glycosidic bond and deuterium label retaining conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collagen alpha1(IV) chain containing triple helical polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1997
                                                                            30-JUN-1993;
27-SEP-1995;
                                                                                                                                        US5576419-A.
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W13024 standard;
                         WPI; 1997-011309/01
                                           Fields
                                                                                                      30-JUN-1993;
                                                                                                                       19-NOV-1996
                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                   Modified-site
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                                                           (MINU ) UNIV
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gvkgdkgnpgwpgap 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                            MINNESOTA
                                                                            93US-0085633.
95US-0534342.
                                                                                                      93US-0085633
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/note=
                                                                                                                                                                                                                                            /label- Hyp
25..39
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                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                        /label- Hyp
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                                                                                                                                                                                                                                                                     'label- Hyp
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                                                                                                                                                                                        "linked via
comprising
sequence"
                                                                                                                                                                         "linked via
                                                                                                                                                                                                                            "collagen alphal(IV) chain residues
1263-1277"
                                                                                                                                                                                                                                                                                   Нур
                                                                                                                                                       comprising sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                peptide bond to Pro39 of peptide residues 1-39 of present
                                                                                                                                                                                                  peptide bond to F
residues 1-39 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell; adhesion; migration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 19;
7.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                          Pro39 of
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                                                                                                                                                                                                                                                                                                                                                                                                                            activity;
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RESULT
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                                                                                                                                                                                                                                                                      Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lung cancer associated protein; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynecological; antlibacterial; diagnosis; neural disorder; immune disorder; reprodu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of triple helical polypeptide (THP-2), which includes a collagen cell adhesion sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 48; Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which may contain collagen cell adhesion sequences, useful for studying structure and biological activity of collagen % \left\{ 1\right\} =\left\{ 1
                                                                                                                                                                         Claim 11; Page 996-998; 1425pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587514/55
N-PSDB; F18045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2000; 2000WO-US05918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferative disorder;
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(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide sequence SEQ ID 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Polynucleotide sequences r17982 - r18424 encode human lung cancer associated proteins represented in B58106 - B58548. Lung cancer associated proteins and polynucleotide sequences, their agonists,

and

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RESULT
R23873
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Best Local :
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Polynucleotide sequences F18425 - F18433 and peptide B58549 are used in the course of the invention for the identification and characterisation
Isolation of DNA encoding alpha-5(IV)polypeptide of type IV collagen - to detect mutations in genes for alpha-5(IV) chain which produce genetic or acquired basement membrane disorders e.g. Alport's syndrome
                                                                                                                                                                                                                                                                            07-JUL-1989;
                                                                                                                                                                                                                                                                                                                         07-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "interruption Misc-difference 334..336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "
Misc-difference 275..277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "interruption in Gly-X-Y sequence" Misc-difference 159..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R23873 standard; Protein; 772 AA
                                                                                                                                                                                   Hostikka SL,
                                                                                                                                                                                                                                                                                                                                                                      19-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                 US5114840-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutations; Alport's
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                                                                                                                                    WPI; 1992-192174/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonists may have neuroprotective; cytostatic; cardioactive;
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                                                                                                                   Q24551.
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6.3e-05;
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RESULT 16
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Best Local
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                                                                                     20-DEC-1990;
07-JUL-1989;
11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of the alpha 5(IV) polypeptide chain of human type IV collagen, the major component of basement membranes. The protien contains the Gly-X-Y repeat coding sequence typical for collagenous proteins at one end and a typical NC-domain coding sequence at the other end. The sequence can be used to detect mutations in individual genes specific for this chain which can, directly or indirectly, produce several human diseases. It can also be used to determine genetic, e.g. Alport's syndrome, or acquired e.g. diabetes mellitus, disorders of the basement membrane, and as probes or antibodies against these nucleotide sequences. Gene fragments generated through amplifications from human genomic or cloned DNA can also be used for detection and analysis of genes.
 Hostikka
                                                                                                                                                 07-JUL-1989;
                                                                                                                                                                              14-JAN-1997.
                                                                                                                                                                                                            US5593900-A.
                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen alpha5(IV); basement membrane; Alport's syndrome; mephritis; kidney; renal failure; antibody; diagnosis; COL4A5 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human type IV collagen alpha-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09643 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig
                             (HOST/) HOSTIKKA S L.
(HOYH/) HOYHTYA M.
(TRYG/) TRYGGVASON K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 gikgekgnpgqpglp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVKGDKGNPGWPGAP 15
 SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
Hoyhtya M,
                                                                                                      90US-0630563
89US-0377238
                                                                                                                                                  89US-0377238
                                                                                      94US-0321084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; 14pp; English.
                                                                                                                                                                                                                                                                                   742..751
                                                                                                                                                                                                                                                                                                              544..772
                                                                                                                                                                                                                                                                                                                            /note= "collagenous domain contains Gly-X-Y
    tripeptide repeats, interrupted at
    positions 43-47, 159-160, 275-276,
    456-459"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1.,543
                                                                                                                                                                                                                                                     /note= "peptide used
                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                      /label= Collagenous_domain
                                                                                                                                                                                                                                                                                               /label= Non-collagenous_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%;
73.3%;
                                                                                                                                                                                                                                 "peptide used to raise diagnostic
antibodies (Claim 1)"
                                                                                                                                                                                                                                                                   Immunogenic_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               772 AA.
 Tryggvason K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 772;
0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence of a portion (W09643) of the previously unknown human type IV collagen chain, alpha5(IV), was deduced from cDNA clones (see also T47812) obtd. using probes based on conserved sequences of human alpha1(IV) and alpha2(IV) collagen chains and of the Drosophila alpha1(IV) chain. It includes a complete non-collagenous domain that shows 83% identity with that of alpha1(IV) and 63% with that of the alpha2(IV) chain. Mutations in the alpha5(IV) gene (COL4A5) are associated with Alport's syndrome. Antibodies raised against a peptide (see also W09644) specific to alpha5(IV) can be used in the diagnosis of basement membrane disorders such as Alport's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                        cardioactive; immunomodulatory; muscular active; vulnerary;
gastrointestinal; nephrotropic; antiinfective; gynecological;
antibacterial; diagnosis; neural disorder; immune disorder; r
                             Claim 11;
                                                                                                                WPI; 2000-587514/55
N-PSDB; F18056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B58180 standard; Protein; 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-2B; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies specific for human type IV collagen alpha5 chain used to detect absence of this chain in patients with renal fai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-099481/09
N-PSDB; T47812.
Polynucleotide sequences F17982 - F18424 encode human lung cancer
                                                                                                                                                          Ruben SM
                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05918
                                                                                                                                                                                                                                                                                                                 WO200055180-A2
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lung cancer associated protein; neuroprotective; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung cancer associated polypeptide sequence SEQ ID 518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 gikgekgnpgqpglp 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVKGDKGNPGWPGAP 15
                                                                   cancer associated gene sequences,
gens, useful for treatment, prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                          Page 1008-1010; 1425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772
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                                                        cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                          disorder;
                                                                                                                                                                                                                               99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                            banow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB Pred. No. 0.03
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                            healing;
                                                                    prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in patients with renal failure
                                                                    referred
tion, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.037;
                                                                                                                                                                                                                                                                                                                                                                            infectious
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                                                                   to as lung
diagnosis (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 772;
                                                                                                                                                                                                                                                                                                                                                                          disorder; reproductive; disease.
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                                                                    g cancer
of disorders
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W40114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, polimonary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences F18425 - F18433 and peptide B58549 are used in the course of the invention for the identification and characterisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated proteins represented in B5810b - B5530
associated proteins and polynucleotide sequences,
                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                COL4A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-1(IV) collagen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W40114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W40114 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the polynucleotide and protein sequences.
                                   Region
                                                                         Region
                                                                                                                  Region
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                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Alports
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 gpkgpkgdpgfpgap 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                               gene; type
syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins represented in B58106 - B58548. Lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                           /note= "This
377..378
                                                                                                                                                                                                                                                                                  /note= "This region 244..257
                                                                                                                   /note= "This
403..404
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
163..171
         /note= "This region interrupts a
                                      467..473
                                                /label- VIII
/note- "This
                                                                                       /note= "This
                                                                                                                                                                                                                                          /note= "This
273..274
                                                                                                                                                                                                                                                                                                                                   note= "This region interrupts a collagenous repeat"
                         label-
                                                                                                     /label= VII
                                                                                                                                                                                   'label-
                                                                                                                                                                                                              note- "This
                                                                                                                                                                                                                            /label-
                                                                                                                                                                                                                                                                                                           label-
                                                                                                                                                                                                                                                                                                                                                   label-
                                                                                                                                             label-
                                                                                                                                                                                                                                                                     'label= III
                                                                                                                                                                                                                                                                                                                                                                                                                                IV collagen protein; alpha-6(IV); alpha-1(IV);
lelomyomatosis; diagnosis; gene therapy; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.6%;
                                                                                                                                                                                                                                                                                                                         . 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64;
Pred. No.
                                                 region
                                                                                       region
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                                                                                                                                                                     region
                                                                                                                                                                                                                                                    region
                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                 interrupts
                                                                                       interrupts a
                                                                                                                             interrupts a collagenous repeat"
                                                                                                                                                                      interrupts a
                                                                                                                                                                                                               interrupts
                                                                                                                                                                                                                                                    interrupts a collagenous repeat"
                                                                                                                                                                                                                                                                                             interrupts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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         collagenous repeat'
                                                collagenous repeat
                                                                                                                                                                                                              collagenous
                                                                                       collagenous repeat"
                                                                                                                                                                      collagenous
                                                                                                                                                                                                                                                                                             collagenous repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                     repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
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US5731192-A

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RESULT
R71704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the human alpha-1(IV) collagen protein which is used to analyse a novel human alpha-6(IV) collagen protein encoded by the COL4A6 gene. The alpha-6(IV) protein can be used for diagnosis or gene therapy of diseases associated with collagen type IV pathology, especially Alport's syndrome and associated diffuse leiomyomatosis. The polypeptide may also be used for generating monoclonal or polyclonal antibodies having specificity for the alpha-6(IV) polypeptide especially an antibody that is not crossreactive with other collagen proteins including alpha-1(IV), alpha-2(IV) and alpha-5(IV) collagens.
  Assaying collagen fragments in
                                                         WPI; 1995-131456/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperthyroidism; bone; rescosteoarthritis; vasculitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen alpha 1 (III) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R71704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R71704 standard; protein; 1078 AA.
                                                                                                          Bonde M,
                                                                                                                                                                                                                                                                               19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                      23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding human alpha-6(IV) collagen diagnosis or gene therapy of Alport's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1993;
                                                                                                                                                                    (OSTE-) OSTEOMETER AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 3; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reeders ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 gdkgekgspgfpgep 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-216495/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVKGDKGNPGWPGAP
                                                                                                          Qvist P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; immunoassay; metabolism; diagnosis; monitoring;
osteoporosis; metastatic progression; Paget's disease;
oidism; bone; resorption; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                           93DK-0001040
                                                                                                                                                                                                                                                                               94WO-DK00348
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Pred. No.
body fluid by
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immunoassay -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 532;

    useful for, e.g.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CCCCCCCXXXX PTTTXX
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Y96125
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PA
PI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                              The present sequence is that of human type III collagen alpha-1. The invention is based on the discovery function is based on the discovery function is particular collagen fragments in body fluids of patients compared with those of healthy subjects. These fragments are generated with those of healthy subjects. These fragments are generated upon collagen degradation and are partly characterised by the
presence of potential sites for crosslinking. A method for assaying collagen fragments in a body fluid sample is based on the competitive binding to immunological binding partners of collagen
                                                                                                                                                    Disclosure; Column 46-51; 41pp; English.
                                                                                                                                                                                                                         Assaying type I collagen fragments for diagnosing osteoporosis in postmenopausal woman, involves contacting body fluid with synthet
                                                                                                                                                                                                                                                                           WPI; 2000-586349/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen type III; vasculitis syndrome; assay; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome). I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis, metastatic progression, Paget's disease, hyperthyroidism or other conditions involving excessive bone resorption; degredation of type II collagen may indicate rheumatoid arthritis or osteoarthritis; and of type III collagen, vacuiltis syndrome). The method can also be used to assess the toxicity of a compound and to test drugs for their effect on collagen metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by immunoassay using antibodies directed against synthetic peptides derived from collagen which contain sites of potential crosslinking. The method is used to diagnose and monitor treatment of disorders of collagen metabolism (degredation of type I collagen may indicate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibodies raised against synthetic peptide(s) contg. potential crosslinking sites, to diagnose and monitor disorders of collagen metabolism, e.g. osteoporosis.
                                                                                                                                                                                                      collagen
                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6110689-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y96125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                           Bonde M,
                                                                                                                                                                                                                                                                                                                                          (OSTE-) OSTEOMETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y96125 standard; Peptide; 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure (Appendix A); Page 55; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determination of collagen fragments in body fluids can be achieved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GVKGDKGNPGWPGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gpkgdkgepggpga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type
                                                                                                                                                                                                      pausal woman, involves contacting body fluid with peptide and antibody and quantifying by competiti
                                                                                                                                                                                                                                                                                                           Qvist P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 III alpha-1
                                                                                                                                                                                                                                                                                                                                                                              94US-0187319
                                                                                                                                                                                                                                                                                                                                                                                                              97us-0963825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1078;
                                                                                                                                                                                                         competitive binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                         synthetic
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RESULT
R79163
ID R7
XX
AC R7
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Tatches 11; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
R28916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                     $\times CCCC\times CTT\times CTT\tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kit for detecting genetic pre-disposition for vascular aneurysms - contains primer to amplify portions of Type III procollagen DNA and detects mutation in standard procollagen DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragments in the sample and of synthetic peptides derived from collagen and containing crosslinkable sites (see y96118-21). When considering the degradation of type III collagen, the assay can be used as a means of identifying the presence of vasculitis syndrome.
       R79163;
                                                    R79163 standard; Protein; 471 AA
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  in the pro-alphal(III)
Q30834-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1 describes the determination of the presence of a mutation in the pro-alphal(III) gene. Primers used in PCR are given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutation; pro-alphal(III); primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type III procollagen (prior art).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig lA-F; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuivaniemi SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09219754-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R28916 standard; Protein; 1196 AA
                                                                                                                                                                      738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591
                                                                                                 22
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                                                                                                                                                                                                                   1 GVKGDKGNPGWPGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVKGDKGNPGWPGA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992-398878/48.
DB; Q30849.
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                                                                                                                                                                    gpkgdkgepggpga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                       1196 AA;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prockop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0696607.
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                                                                                                                                                                         751
                                                                                                                                                                                                                                                                                         65.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.2%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                         Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tromp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                               13;
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                                                                                                                                                                                                                                                                                                               Length 1196;
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                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT
Y44171
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                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                residue bovine alpha 3 (IV) collagen protein sequence, a 68 bp bovine genomic fragment was amplified. This fragment was then used to a bovine lens cDNA library and a 1.5 kb partial cDNA clone was obtd. (clone KMCI5). This encodes 238 residues of the triple helical collagenous domain and all 233 residues of the C-terminal non-collagenous (NC1) domain of the alpha 3 (IV) chain. An isolated and substantially pure nt. having the sequence in 096290 is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNAs encoding human or bovine alpha-3 type 4 collagen peptide(s) useful for detection and therapeutic removal of antibodies associated
                                                                                                   Recombinant; bovine; alpha3 chain; type IV collagen; detection; Goodpasture syndrome; antibody; blood; tissue; human; nephrotrophism.
                                                                                                                                                               01-FEB-2000
                                                                                                                                                                                     Y44171;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Columns 5-8; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q96290
                                 26-OCT-1999.
                                                       US5973120-A
                                                                                                                                       Bovine type IV collagen alpha3 chain protein.
                                                                                                                                                                                                           Y44171 standard; Protein; 471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with Goodpasture syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-262631/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hudson BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type IV collagen; alpha 3 chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIV ) UNIV KANSAS MEDICAL CENT (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                    116 gmkgkkgnsgfpgpp
                                                                                                                                                                                                                                                                                 1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the PCR with primers derived from each end of the known 27
                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of bovine alpha
                                                                                                                                                                                                                                                                                                                                                                              471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrison
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0621091
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                                                                                                                                                                                                                                                                                                                               64.18;
66.78;
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                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                               Score 59; DB 1
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 chain of type IV collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ST
                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                         Length 471;
                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                    Gaps
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07-MAR-1995;

95US-0399889

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RESULT
Y56783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                    Disclosure; Columns 19-24;
                                         Diagnosing and treating Goodpasture syndrome using from type IV collagen \, \cdot \,
                                                                                                          Hudson BG,
                                                                                                                                                                30-NOV-1990;
07-MAR-1995;
                                                                                                                                                                                               07-OCT-1998;
                                                                                                                                                                                                                                         US6007980-A
                                                                                                                                                                                                                                                               Bos sp
                                                                                                                                                                                                                                                                                   Goodpasture syndrome; type IV collagen; alpha3 chain; bovine
                                                                                                                                                                                                                                                                                                          Bovine alpha3
                                                                                                                                                                                                                                                                                                                                                      Y56783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a recombinant bovine alpha3 chain of type IV collagen polypeptide. The sequence corresponds to the 238 amino acids of the C-terminal end of the triple helical domain and all 233 amino acids of the C-terminal non-collagenous domain. Alpha3 chain collagen polypeptides are useful for detecting Goodpasture antibodies in blood or tissue from a human patient and for treating Goodpasture syndrome, especially by neutralising the antibodies in the blood. The polypeptides
                                                                                                                                                                                                                     28-DEC-1999
                                                                                                                                                                                                                                                                                                                              27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     also have a nephrotrophic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 31-34; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis
                                                                                                                                                                                                                                                                                                                                                                         Y56783 standard; Protein; 471 AA
                                                                                                                             (UNIV ) UNIV KANSAS MEDICAL CENT.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hudson BG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated alpha 3 chain of type IV collagen polypeptide useful for
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(UNIV ) UNIV KANSAS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVKGDKGNPGWPGAP 15
                                                                         2000-096371/08
DB; 246728.
                                                                                                                                                                                                                                                                                                                                                                                                                              gmkgkkgnsgfpgpp 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 AA;
                                                                                                         Reeders
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95US-0399889.
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66.7%;
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                   26pp;
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Pred. No. 0.62;
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                    English.
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Best Local Similarity
                                        A method has been developed for the detecting liver disease. The method comprises: (a) reacting a patient sample with antibodies (Ab) specific for collagen type XVIII (Coll8); (b) measuring the amount of Ab-antigen complex (C) formed as indicator of the amount of Coll8 present; (c) similar analysis of a non-diseased control; and (d) comparing the amounts of Coll8 in the two samples to detect presence or progression of disease. Elevated levels of Coll8 are: (1) indicative of disease, specifically cirrhosis; and (ii) predictive of the prognosis of disease, specifically hepatocellular carcinoma (there is a relationship between Coll8 mRNA levels and tumour size and necrosis, and survival times are significantly higher in patients with higher Coll8 levels). The method provides non-invasive, early and accurate diagnosis of liver disease. The present sequence represents the sequence common to mouse alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the fluid of a patient by contacting it with a peptide comprising a most 218 amino acids of the human alpha3 chain type IV collagen that contains the fragment shown in Y56785. The methods are useful for the diagnosis and treatment of Goodpasture syndrome. The present sequence represents the bovine alpha3 chain of type IV collagen.
                                                                                                                                                                                                                                                                                                    especially
                                                                                                                                                                                                                                                                                                                                                                                                   Clement B,
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                                                                                                                                                                                                                                                                                                                 XVIII levels - with elevated levels indicative of disease
                                                                                                                                                                                                                                                                                                                                  Diagnosis and monitoring of liver disease by measuring collagen type
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                              (XVIII) collagen chain
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(FIBR-) FIBROGEN INC.
(INRM ) INST NAT SANTE & RECH MEDICALE.
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Query Match 63.0%; Score 58; DB 20; Length 1288;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GVKGDKGNPGWPGAP 15
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Db 300 gmkgqkgepgapgpp 314

Search completed: May 23, 2001, 16:16:14
Job time: 85 sec
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Result
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Maximum DB
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92
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US-08-931-820-4
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Sequence 47, Appl	Sequence 61, Appl	Sequence 4, Appli	Sequence 47, Appl	Sequence 59, Appl	Sequence 17, Appl	Sequence 45, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 1, Appl:	Sequence 20, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

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; MOLECULE TYPE: p
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; STRAIN: IV-H1
US-08-394-748A-1
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US-08-394-748A-1
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                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/394,748A FILING DATE: 27-FEB-1995 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/203,458 FILING DATE: 28-FEB-1994 ATTORNEY/AGENT INFORMATION: NAME: Carter, Charles G.
                                                                                                                                               TELEPHONE: 612-332-53
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6013628west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method for Treating Conditions of the TITLE OF INVENTION: Using Polypeptides NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
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                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                        NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
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                                                                                                    Sequence 1, Application PC/TUS9502478 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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            TITLE OF INVENTION: Met
TITLE OF INVENTION: Of
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0:
FILING DATE: 23-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rela
                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 115 CTTY: MINNEAPOLIS
   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                         l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIELDS, GREGG B.
VENTION: SELF-ASSEMBLING AMPHIPHILES FOR
VENTION: CONSTRUCTION OF PEPTIDE SECONDARY STRUCTURES
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                               linear
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: Floppy disk
IBM PC compatible
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                                                         Method for Treating Conditions
Of the Eye Using Polypeptides
                                                                                                                                                                                                                                                                    100.0%; Score 92; DB 3; 100.0%; Pred. No. 1.6e-07;
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Pred. No. 1.6e-07
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Query Match
Best Local Similarity
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US-08-534-342-3
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Best Local Similarity
Matches 15; Conserv
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                                                                  TELEFAX: 612-332-9081 INFORMATION FOR SEQ ID NO:
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                                                  SEQUENCE CHARACTERISTICS:
                                                                                                  TELEPHONE: 612-332-5300
                                                                                                                                                               FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/085,633
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,342
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
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LENGTH: 15 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 28-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                              TELEPHONE: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Minneapolis
STATE: MN
TOPOLOGY:
                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                NAME: Mueting, Ann M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                 LENGTH:
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                                 24 amino acids
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3100 No. 5576419west Center
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WENTION: mild Solid-Phase Synthesis of Aligned.
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 unknown
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PatentIn Release #1.0, Version #1.25
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Pred. No. 1.6e-07;
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Score 92; DB 1; Pred. No. 2.7e-07;

Length 24;

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Best Local S
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                                                                                                                                                                               Sequence 2, Application US/08534342 Patent No. 5576419
                                                                                          GENERAL INFORMATION:
APPLICANT: Fields, Gregg B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned.
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fields, Gregg B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned.
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08 FILING DATE: 03-JUL-1996 CLASSIFICATION: 525
                 COUNTRY:
                              STATE: MN
                                              CITY: Minneapolis
                                                               STREET:
                                                                                                                                                                                                                                                                                  10 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mueting, Ann M.
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                                                                              DDRESSEE:
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15; Conserv
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3100 No. 5576419west Center
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3100 No. 5726243west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 amino acids
                 USA
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US-08-675-140-2
                             TELEPHONE: 612-332-530
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ZIP: 55402
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; TOPOLOGY: unknown US-08-534-342-2
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08675140 Patent No. 5726243
                                                   FILING DATE: 03-JUL-1996
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 612-332-530
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned, NUMBER OF SEQUENCES: 13
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PRIOR APPLICATION NAME: US 08/085,633
FILING DATE: 30-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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LENGTH: 39 amino acid:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
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                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mueting, Ann M. REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Merchant & Gould STREET: 3100 No. 5726243west Center
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                                                                                                                                                                                                                                                 PatentIn Release #1.0,
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                                       600.253-US-01
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Pred. No.
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APPLICATION.
APPLICATION.
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION DATA:
PAPLICATION UNBER: US 08/085,633
APPLICATION UNBER: US 08/085,633
ATTORNEY, AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION UNBER: 33,977
REFERENCE/DOCKET NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.253
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TT.EFPAX: 612-332-9081
TT.EFPAX: 612-332-9081
TT.EFPAX: 612-332-5001
                                                          US-08-534-342-6
; Sequence 6, Application US/08534342
; Patent No. 5576419
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                                                                                                                                                                                                                         Query Match

Best Local Similarity 73.3

Matches 11; Conservative
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Best Local Similarity
Matches 15; Conserv
                                              GENERAL INFORMATION:
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        APPLICANT: Fields, Gregg B.
TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES:
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TITLE OF INVENTION: Mild
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                                                                                                                                                                                                                                                                                                                                         TYPE: ami
TOPOLOGY:
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                                                                                                                                                                     25 GVXGXXGXPGWPGAP 39
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3100 No. 5576419west Center
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Solid-Phase Synthesis of Aligned
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Pred. No.
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Pred. No. 4
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4.5e-07;
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RESULT 10
US-08-675-140-5
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Best Local Similarity
Matches 11; Conserv
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NAME: MUCKING, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
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                                                                                                                                                                                              ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                    APPLICATION NUMBER: US/08/675,140
FILING DATE: 03-JUL-1996
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-JUN-1993
                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fields, Gregg B. TITLE OF INVENTION: Mild Solid-Phase Synthesis of Aligned,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
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APPLICATION NUMBER: US 08/085,633
FILING DATE: 30-JUN-1993
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                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3100 No. : CITY: Minneapolis
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                                                                                                                                                                                                                                                                                           CITY: Minneapolis
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3100 No. 5726243west Center
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3100 No. 5576419west Center
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SYSTEM: PC-DOS/MS-DOS
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73.3%;
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Pred. No. 0.0024;
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RESULT
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                                                                                                                  Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                  TELEFAX: 612-3:
INFORMATION FOR SEQ
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 00 FILING DATE: 30-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/085,633
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fields, Gregg
TITLE OF INVENTION: Mild
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                           25 GVXGXXGXPGWPGAP
                                                                                                                Local
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                         NAME: Mueting, Ann M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/675,140 FILING DATE: 03-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Minneapolis
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                                                                       1 GVKGDKGNPGWPGAP 15
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                                                                                                                Similarity
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3100 No. 5726243west Center
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                                                                                                                71.78;
73.38;
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73.3%;
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                                                                                                                Score 66; DB 1; Pred. No. 0 0024;
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Pred. No. 0.0024;
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                                                                                                                              DB 1; Length 39;
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US-08-494-168-9

; Sequence 9, Application US/08494168

; Patent No. 5731192
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 00 FILING DATE: 27-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: SAXE, Bernhard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                   TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                         293 GDKGEKGSPGFPGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                               APPLICATION NUMBER:
                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
               FILING DATE:
                                                                                 FILING DATE:
                                                                                                 APPLICATION NUMBER:
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TELEX: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3000 K Street, N.W., ashington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                 EP 96202596.1
                                                                                                  US/08/931,820
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Pred. No. 0.19;
3; Mismatches
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Best Local Similarity 78.6%;
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                                                                                                         TELEFAX: 212-753-6237
TELEX: 236687
NFORMATION FOR SEQ ID NO:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-527-7700 TELEFAX: 212-753-6237
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INCOMMATION:
NAME: Gogoris, Adda C
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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LENGTH: 1057 amino acids
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590 GPKGDKGEPGGPGA 603
                                                                                                                                                                                               NAME: GOGORÍS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 436
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LOCATION: 1055
OTHER INFORMATION: /labe
OTHER INFORMATION: /note
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STRANDEDNESS: Sir
                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
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                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08963825
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linear
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                                 linear
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               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Modified
/note= "Ala may be Pro"
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Pred. No. 0.54;
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; LENGTH: 471
; TYPE: PRT
; ORGANISM: Calf
US-09-167-364-24
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US-08-399-889-24
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Best Local Similarity
Watches 11; Conserva
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US-08-963-825-21
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Best Local Similarity
Matches 10; Conserv
Query Match
Best Local Similarity
Matches 10; Conserv
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CURRENT FILING DATE: 1995-03-07
EARLIER APPLICATION NUMBER: 07/621091
EARLIER FILING DATE: 1990-11-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 24.
                                                                                                                                                           SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Appli
Patent No. 6007980
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APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 951263B
FILE REFERENCE: 951263B
                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/399889
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/167,364
CURRENT FILING DATE: 1998-10-07
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APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 951263A
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                                                                                                                                                                               SOFTWARE: PatentIn
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TYPE: PRT
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     Conservative
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                  64.18;
66.78;
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78.6%;
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66.78;
 Score 59; DB 3; Pred. No. 0.32; 2; Mismatches
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Pred. No. 0.55;
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Pred. No. 0.32;
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                                    Length 471;
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     Indels
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116 GMKGKKGNSGFPGPP 130

1 GVKGDKGNPGWPGAP 15

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                                                                                Sequence 7, Application US/09249200 Patent No. 6197931
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Best Local Similarity
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                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,795
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gross, Mitchell
APPLICANT: Lysko, Paul
TITLE OF INVENTION: Human Macro Scavenger Rec
TITLE OF INVENTION: eptor
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                    APPLICANT:
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                 PPLICANT:
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 PPLICANT:
                                                                                                                                                                                     265 GVKGDQGKPGVQGVP 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-4026
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                                                                                                                                                                                                        1 GVKGDKGNPGWPGAP 15
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amino acid
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ADAMOU, JOHN
GROSS, MITCHELL
LYSKO, PAUL
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                                               ELSHOURBAGY, NABIL
                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                      60.98;
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Pred. No. 0.91;
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                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                    Length 489;
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
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; Sequence 2, Applic

; Patent No. 5691197
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                                                                                                                            ; TITLE OF INVENTION: A
FITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,200
FILING DATE: 12-FEB-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/794,795
FILING DATE: 04-FEB-1997
APPLICATION NUMBER: 60/017,699
FILING DATE: 23-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: PRESEL1A, Paul F
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN MARCO SCAVENGER RECEPTOR NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELLEFAX: 610
TELEFAX: 846169
                                                                                                                                                                                                                                                                                                                                                                                                265 GVKGDQGKPGVQGVP 279
                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Prestla, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG-50009-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box your CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                              ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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        Cleveland
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Ohio
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                             1100 Superior Avenue Suite 700
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Elomaa, Outi
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O. Box 980
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                                                                                                                            No. 5691197el Macrophage Receptor with a Collagenous Domain and the Polypeptide Chain Encoded by such a Sequence
                                                                                                                                                                                                             An Insolated DNA Sequence For a

    Mismatches

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Pred. No. 0.91;
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U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
MEDIUM TYPE: 720 Kb storab

3.50 inch,

IBM PS/2,

Model 35 SX

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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 518 aming
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Patent No.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/392
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105682
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                   COMPUTER: IBM PS/2, Model 3
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 incl
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Ins
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 GYKGDQGKPGVQGVP 308
                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 44114-2518
                                                                                                                                                                                                                                              CITY: Cleveland
STATE: Ohio
                                                      FILING DATE:
                                                                                                                                                                                                                                                                                STREET: 1100 Superior Avenue STREET: Suite 700
                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee
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66.7%;
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                                                                     US/08/893,467A
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                                                                                                                                                                       3.50 inch,
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Pred. No.
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Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
                                                                                                                                                                                                                                                                    FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                          TELLETAX: (-... 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 GVKGDQGKPGVQGVP 308
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CITY: Washington, D.C.
                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08494168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Foley & Lardner 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (216)
                                                                                                                                                                                    (202)672-5399
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66.7%;
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Pred. No. 0.
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0.96;
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4 GDKGNPGWPGAP 15

Conservative

60.9%; 75.0%;

Score 56; Pred. No.

DB

Length 546;

Indels

0,

Gaps

0

Mismatches

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168 GPKGNPGYPGPP 179

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RESULT 24
US-08-494-168-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Bovine
US-09-011-735-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-011-735-J
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                                                                                          Sequence 2, Application US/08494168 Patent No. 5731192
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09011735B Patent No. 6110708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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SEQ ID NO 2
LENGTH: 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wakamiya, No. 6110708utaka TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof FILE REFERENCE: 19036/34548 CURRENT APPLICATION NUMBER: US/09/011,735B CURRENT FILING DATE: 1998-05-22 EARLIER APPLICATION NUMBER: JP 7-209698 EARLIER FILING DATE: 1995-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wakamiya, No. 6110708utaka
TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof
FILE REFERENCE: 19036/34548
CURRENT APPLICATION NUMBER: US/09/011,735B
CURRENT FILING DATE: 1998-05-22
                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: JP 7-209698
EARLIER FILING DATE: 1995-08-17
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
APPLICANT: Reeders, St
APPLICANT: Zhou, Jing
TITLE OF INVENTION: CC
TITLE OF INVENTION: 01
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112 GLKGEKGAPGETGAP 126
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les 10; Conserv
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                                                    Reeders, Stephen T.
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Collagen COL4A6: Gene, Protein and Method of Detecting Collagen Deficiency
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66.7%;
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Pred. No. 0.89;
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Pred. No. 0.42;
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RESULT 25
US-09-219-849-38
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Best Local Similarity
Matches 9; Conserv
                                                                                                   SOFTWARE:
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38,
                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 2728
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                         atent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/112
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 4039
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                  ORGANISM: Artificial Sequence
                                                                      TYPE: PRT
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid sequence
                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              749 GPRGEKGLPGFPGLP 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy dis)
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T: 3000 K Street, N.W., Suite 500
Washington, D.C.
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                                                                                                                       PatentIn Ver.
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MOOBROEK, ANDREAS
WERTEN, MARC W.T.
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                                                                                                                                                                                                        SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.8%;
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Pred. No. 4.6;
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US-09-219-849-38

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Query Match

Best Local Similarity 60.0%; Pred. No. 0.79;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GVKGDKGNPGNPGAP 15

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Db 125 GDRGENGSPGAP 139

Search completed: May 23, 2001, 16:16:26

Job time: 76 sec
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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    protein search, using sw model
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1: pir1:*
2: pir2:*
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Match Length
    198801 seqs, 68722935 residues
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Gapop 10.0 , Gapext 0.5
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92
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collagen a 
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RESULT 1 OHEAN STATEMENTS RESULT 1 OHEAN STATEMENT SHOWS SHOWN STATEMENTS RESULT 1 OHEAN STATEMENT SHOWS SHOWN SHOWN STATEMENT SHOWN

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R;MacWright, R.S.; Benson, V.A.; Lovello, K.T.; van der Rest, M.; Fietzek, P.P.
Blochemistry 22, 4940-4948, 1943
A;Title: Isolation and characterization of pepsin-solubilized human basement membrana, Reference number: S16910; MUID:84053346
A;Molecule ****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Restricted homology between human alpha-1 type IV and other procollagen chains A;Reference number: S16879; MUID:85216555
A;Accession: S16879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 534-718, 'D',720-836,'Y',838-841,'P',843-903,'Q',905-913,'K',915-997,'K',999-
A;Experimental source: placenta
R;Glanville, R.W.; Rauter, A.
Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1981
A;Title: Pepsi's fragments of human placental basement-membrane collagens showing interrula; Reference number: S18908; MUID:82005835
A;Accession: A58517
                                                                                                                                                                        A;Title: The arrangement of intra- and intermolecular disulfide bonds A;Reference number: S02550; MUID:89005112 A;Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1435-1461,'M',1463-1482,'X',1484-1491;1501-1514,'X',1516-1519;1534-1553,'X'
R;Siabold, B; Deutzmann, R.; Kuehn, K.
Eur. J. Biochem. 176, 617-624, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Oberbaeumer, I.; Laurent, M.; Schwarz, U.; Sakurai, Y.; Yamada, Y.; Vogeli, G.; Voss, Eur. J. Blochem. 147, 217-224, 1985
A;Title: Amino acid sequence of the non-collagenous globular domain (NC1) of the alpha-A;Reference number: A02864; MUID:85127033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:M10940; NID:g180421; PIDN:AAA52006.1; PID:g180424 R;Brinker, J.M.; Gudas, L.J.; Loidl, H.R.; Wang, S.Y.; Rosenbloom, J.; Kefalides, Proc. Natl. Acad. Sci. U.S.A. 82, 3649-3633, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 534-537,'G',539,'G',541-542,'G',544-549;939-940,'M',942-944,'V',946,'X',948-A;Experimental source: placenta
R;Plhlajaniemi, T.; Tryggvason, K.; Myers, J.C.; Kurkinen, M.; Lebo, R.; Cheung, M.C.; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 143, 545-556, 1984
A;Title: Structure of human-basement-membrane (type IV) collagen. Complete amino-acid
A;Reference number: A02863; MUID:85003629
A;Accession: A02863
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A; Residues: 371-554 <EBL>
R; Babel W.; Glanville, R.W.
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A;Reference number: S39614;
A;Accession: S39614
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A;Map position: 13q34-13q34
A;Introns: 28/3; 48/3; 78/3; 93/3; 108/3; 129/3; 147/3; 156/3; 184/3; 205/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:M11315; NID:g180817; PIDN:AAA52042.1; PID:g180818 R;Oberbaeumer, I.; Laurent, M.; Schwarz, U.; Sakurai, Y.; Yamada, Y.; Voge
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A; Residues: 1256-1669 <PIH>
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A; Accession: S01466
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A;Cross-references: EMBL:Y00706; NID:g2954;
R;Ebbe, J.A.; Golbik, R.; Mann, K.; Kuehn,
EMBO J. 12, 4795-4802, 1993
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                                                                          A;Cross-references: GDB:119791; OMIM:120130
                                                                                                            A; Gene: GDB: COL4A1
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A; Residues: 1259-1669 <BRI>
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A; Title: cDNA clones coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUID:85207819
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K.; Kuehn, K.
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                                                                                                                            A; Accession type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1669 < MUT>
A; Cross-references: EMBL: J04694; NID: g556296;
A; Cross-references: EMBL: J04694; Ogell, G.
                R:Muthukumaran, G.; Blumberg, B.; Kurkinen, J. Biol. Chem. 264, 6310-6317, 1989
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nes 15; Conser
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A;Description: structural component of extracellular basement membrane C;Superfamily: collagen alpha 1(IV) chain C;Keywords: basement membrane; blocked amino end; cell binding; coiled F;1-26/Domain: signal sequence #status predicted <SIG>F;27-1669/Product: collagen alpha 1(IV) chain #status predicted <MAT>F;29-162/Domain: amino-terminal nonhelical, 7S <7SD>F;29-162/Domain: amino-terminal nonhelical, 7S <7SD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;414-452/Region: integrin binding #status experimental F;597-599/Region: cell attachment (R-G-D) motif F;917-919/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;163-1440/Domain: interrupted helical <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /1; 731/3; 782/1; 820/1; 876/1; 906/1; 957/1; 990/1; 1020/1; 1066/3; 1109/1; 1136/1; C;Complex: type IV collagen is a heterotrimer of two alpha 1(IV) chains and one alph ociations among trimer amino-terminal domains (disulfide and desmosine cross-links).
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Conservative
                  100.0%;
15
            0;
                  Score 92;
Pred. No.
                   1.2e-05;
                        DB
                       Length 1669
            Indels
            0,
            Gaps
            0;
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collagen alpha 1(IV) chain precursor mouse

3 A32003; A31766;

J. Biol. Chem. 264, 6310-6317, 1989
A;Title: The complete primary structure for A;Reference number: A33525; MUID:89197932
A;Accession: A33525 the alpha-1-chain of mouse collagen

PIDN:AAA50292.1; PID:g556297

derived amino

acid sequence

of.

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A;Molecule type: DNA
A;Residues: 1-28 <KAY>
A;Cross-references: EMBL:J04448; NID:g192666; PIDN:AAA37437.1;
A;Cross-references: EMBL:J04448; NID:g192666; PIDN:AAA37437.1;
R;Burbelo, P.D.; Martin, G.R.; Yamada, Y.
Proc. Natl. Acad. Sci. U.S.A. 85, 9679-9682, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 9679-9682, 1988
A;Title: Alpha1(IV) and alpha2(IV) collagen genes are regulated A;Reference number: A94220; MUID:89071759
A;Accession: A31766
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   R;Schuppan, D.; Timpl, R.; Glanville, R.W. FEBS Lett. 115, 297-300, 1980
A;Title: Discontinuities in the triple helical sequence Gly-X-Y of A;Reference number: S16909; MUID:80246483
A;Accession: S16909
                                                                                                                                                                                                                                            A;Cross-references: EMBL:M23333; NID:g340878; PIDN:AAA51625.1; PID:g535668 R;Sakurai, Y; Sullivan, M.; Yamada, Y.
J. Blol. Chem. 261, 6654-6657, 1986
A;Title: Alpha-1 type IV collagen gene evolved differently from fibrillar A;Reference number: S19094; MUID:86196099
A;Accession: S19094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: EMBL:J03944; NID:g192673; PIDN:A R:Kaytes, P.; Wood, L.; Therlault, N.; Kurkinen, M.; J. Biol. Chem. 263, 19274-19277, 1988
A:Title: Head-to-head arrangement of murine type IV A:Reference number: A92702; MUID:89066738
A:Accession: A32003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:M15832; NID:g192282; PIDN:AAA37340.1; R;Killen, P.D.; Burbelo, P.D.; Martin, G.R.; Yamada, Y. J. Biol. Chem. 263, 12310-12314, 198
A;Title: Characterization of the promoter for the alpha-1(IV) careference number: S19079; MUID:88315019
A;Accession: S19079
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Eur. J. Blochem. 147, 217-224, 1985
A;Title: Amino acid sequence of the non-collagenous
A;Reference number: A02864; MUID:85127033
A;Accession: A02864
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J. Blol. Chem. 263, 8706-8709, 1988
A;Title: Structure of the amino-terminal portion of the murine alpha-1(IV) collagen A;Reference number: A28066; MUID:88243724
A;Accession: A28066
                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1110-1135;1189-1316;1342-1383;1418-1487
A; Cross-references: EMBL:M13027
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A; Residues: 1-28 <BUR>
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A; Residues: 1441-1669 < KUR>
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A; Residues: 1276-1669 <OBE>
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R;Oberbaeumer, I.; Laurent, M.; Schwarz, U.; Sakurai, Y.; Yamada, Y.; Voge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-28 <KI2>
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Residues: 1-129 <KI1>
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Residues: 1-185,'L',187-318,'S',320-368,'L',370-402,'F',404-480,'L',482-492,'H',494-7
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en, M.; Vogeli, G.
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A; Molecule type: protein
A; Residues: 1-9 <GUZ>
R; Schuppan, D.; Glanville, R.W.;
Blochem. J. 220, 227-233, 1984
A; Title: Sequence comparison of
A; Reference number: S16907; MUID
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A; Title: Subunit Structure and assembly of the globular domain of basement-membrane ch; Accession: S17801
A; Molecule type: protein
A; Rolecule type: protein
C; Genetics:
A; Rolecule type: protein
C; Rolecule type: protein
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C; Rolecule type: protein
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1173-1181, 'X',1183-1184, 'X',1186-1187, 'X',1189-1205, 'Q',1207, 'XE',1210-12
3, 'SP',1266, 'IT',1269, 'SK',1272, 'DM';1275, 'L',1277-1282;1316-1318, 'X',1320-1327, 'X',1
R; Weber, S.; Engel, J.; Wiedemann, H.; Glanville, R.W.; Timpl, R.
Eur. J. Biochem. 139, 401-410, 1984
A; Title: Subunit structure and assembly of the globular domain of basement-membrane c
A; Title: Subunit structure and assembly of the globular domain of basement-membrane c
A; Reference number: S17801; MUID:84132058
                                             collagen alpha 1(IV) chain - bovine (fragments) c;Species: Bos primigenius taurus (cattle) c;Date: 04-Dec-1992 #sequence_revision 05-Apr-1995 #t. C;Accession: A39474; S16907; S18432; A39419 R;Gunwar, S.; Noelken, M.E.; Hudson, B.G. J. Biol. Chem. 266, 14088-14094, 1991 A;Title: Properties of the collagenous domain of the le helical structure and noncollagenous domain. A;Reference number: A39474; MUID:91310700
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A;Residues: 940-946, 'G', 948-949, 'G', 951-955, 'G', 957;1213-1228, 'x',1230-1234, 'p',1236-
R;Schuppan, D.; Glanville, R.W.; Timpl, R.
Eur. J. Biochem. 123, 505-512, 1982
A;Title: Covalent structure of mouse type-IV collagen. Isolation, order and partial a A;Reference number: A25991; MUID:82186723
A;Recession: A25991
A; Reference number: A39474;
A; Accession: A39474
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A; Residues: 940-946, 'X', 948-949, 'X', 951-955, 'X', 957-964, 'X', 966-991, 'X', 993-1003, 'X', 61, 'X', 1063-1065, 'X', 1067-1080, 'X', 1082-1083, 'X', 1085-1106, 'X', 1108-1115, 'DE', 1118-11
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Best Local
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13; Conserv
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Pred. No. 0.0014;
0; Mismatches
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n of pepsin-resistant segments MUID:84256630

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A;Cross-references: GB:Z37153; NID:g587203; PIDN:CAA85512.1; PID:g587204 R;Pihlajaniemi, T.; Pohjolainen, E.R.; Myers, J.C. J. Biol. Chem. 265, 13758-13766, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 21-Jul-2000
C;Accession: S22917; A54355; A57079; A37122; I54317; A34850; S18850; I56971;
R;Zhou, J; Hertz, J.M.; Leinonen, A; Tryggvason, K.
J. Biol. Chem. 267, 12475-12481, 1992
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A;Residues: 337-347, 'FL', 350-356 <GU3>
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
E;31,34,37,46,61,69,78,84,87,102,110,122,125,137,140,143,149,155,158,161,164,185,188,199
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Mesidues: 4-8, E',10-68;69-158;159-321;322-349 <SC2>
A;Besidues: 4-8, E',10-68;69-158;159-321;322-349 <SC2>
R;Butkowski, R.J.; Langeveld, J.P.M.; Wieslander, J.; Hamilton, J.; Hudson, B.G.
J. Biol. Chem. 262, 7874-7877, 1987
A;Title: Localization of the Goodpasture epitope to a novel chain of basement membrane
A;Reference number: S18432; MUID:87222419
A;Accession: S18432
                                                                                                                                                                                                                                                                                                                       A; Title: Deletion of the paired alpha5(IV) A; Reference number: A57079; MUID:93361972 A; Accession: A57079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Zhou, J.; Leinonen, A.; Tryggyason, K.
J. Biol. Chem. 269, 6608-6614, 1994
A;Tille: Structure of the human type IV collagen
A;Reference number: A54365; MUID:94165049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 5(IV) chain precursor, renal splice form - human N;Alternate names: procollagen alpha 5(IV) chain N;Contains: collagen alpha 5(IV) chain precursor, leukocyte splice
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A;Title: Glomerular basement membrane. Identification of dimeric subunits A;Reference number: A39419; MUID:91332055
A;Accession: A39419
                                                                                            A; Accession: A37122
                                                                                                                   A; Title: Complete primary structure of the triple-helical A; Reference number: A37122; MUID:90337990
                                                                                                                                                                                                                                                                                                                                                                                                       R; Zhou, J.; Mochizuki, T.; S
Science 261, 1167-1169, 1993
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A; Residues: 1-922 <ZH2>
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A; Residues: 1-967 < ZHO>
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A; Residues: 337-347, 'FL', 350-353 <BU2>
R; Gunwar, S.; Ballester, F.; Kalluri,
                                                                 A; Molecule type: mRNA
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  ;Residues: 84-439,'GS',442-624,'LALQ',629-666,'FR',669-887,'R',889-1264,1271-1691 <PIH>;Cross-references: GB:J05558; EMBL:M58526; NID:g1314209
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:U04470; NID:g463378; GB:U04520; NID:g463428; PIDN:AAC27816.1; PII; Chou, J.; Mochizuki, T.; Smeets, H.; Antignac, C.; Laurila, P.; de Paepe, A.; Tryggvas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A54365
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete amino acid sequence of the human alpha-5(IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               Smeets,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                             and alpha6(IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN: AAA52046.1;
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0.0023;
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A;Cross-references: GB:S65767; NID:g425563; PIDN:AAD13967.1; PID:g4261667 A;Note: frameshift mutation from a patient with Alport syndrome; five other mutations C;Comment: Prolines and lysines at the third position of the tripeptide repeating uni
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A;Cross-references: GB:S75903; NID:g913882; PIDN:AAB33374.1; PID:g913883 A;Note: permature termination mutation from a patient with Alport syndrome; R;Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Try9 Genomics 17, 485-489, 1993 Genomics 17, 485-489, 1993 Four movel mutations in the COL4A5 gene of patien A;Title: Identification of four movel mutations in the COL4A5 gene of patien A;Reference number: 154188; MUID:94010948
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 924-1264,1271-1691 <ZH3>
A; Residues: 924-1264,1271-1691 <ZH3>
A; Residues: 924-1264,1271-1691 <ZH3>
A; Cross-references: EMBL:M63455; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AAA51558.1;
B; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AAA51558.1;
B; EMBL:M63470; EMBL:M63471; EMBL:M63472; EMBL:M63473; NID:g177922; PIDN:AAA51588.1;
J.J.
                                                                                                                                                                                                                                                                                                                                                                                                               R; Nakazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Kidney Int. 46, 1307-1314, 1994
A;Title: Mutations in the COL4A5 gene in Alport syndrome: A;Reference number: I56975; MUID:95156893
A;Accession: I56975
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A;Residues: 313-324, "E', 326-330 <REN>
A;Cross-references: GB:S59334; NID:g299946; PIDN:AAD13909.1; PID:g4261609
R;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Try
Proc. Natl. Acad. Sci. U.S.A. 87, 1606-1610, 1990
A;Title: Identification of a distinct type IV collagen alpha chain with re
A;Reference number: A34850; MUID:90160375
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A;Title: De novo mutation in the COL4A5 gene converting A;Reference number: I54317; MUID:93244772
A;Accession: I54317
A; Molecule type: DNA
A; Residues: 1604-1607, 'VHDAYKC' <LEM>
                                                                  A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1595-1602 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1448-1477 < MYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, Am. J. Hum. Genet. 46, 1024-1033, 1990
A;Title: Molecular cloning of alpha5(IV) collagen and A;Reference number: A35335; MUID:90252791
A;Accession: A35335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S69169; NID:g545097; PIDN:AAC60613.1; A;Note: frameshift mutation in patient with Alport syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S69168; NID:g545095; A;Note: kidney splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1258-1276 <GUO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Differential splicing of COL4A5 mRNA A;Reference number: I56971; MUID:94133540 A;Accession: I56971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomics 9, 1-9, 1991
A;Title: Characterization of the 3' half of the human
A;Reference number: A37969; MUID:91169491
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A; Residues: 914-1264,1271-1691 <HOS>
A; Cross-references: EMBL:M31115; NID:g180824; PIDN:AAA52045.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: submitted to the EMBL Data Library, February 1991 A; Note: the authors translated the codon GCC for residue 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDBJ
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A. Map position: XQ22-XQ22

A. Map position: XQ22-XQ22

A. Introns: 27/3; 47/3; 77/3; 92/3; 107/3; 128/3; 105/3; 182/3; 203/3; 215/3; 229/

A. Introns: 27/3; 47/3; 77/3; 92/3; 1006/1; 1006/1; 1036/1; 1185/1; 1185/1; 1185/1; 1

A. Mote: the alpha 5(IV) and alpha 6(IV) chain genes are encoded on opposite strands with C:Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha 5( mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a er associations in the interrupted helical domain (with disulfide and desmosine cross-links), consecription: minor structural component of extracellular basement membrane C:Superfamily: collagen alpha 1(IV) chain

C:Keywords: Alport syndrome; basement membrane; colled coll; extracellular matrix; glycd F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-169/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <MATIF:27-169/Product: collagen alpha 5(IV) chain, renal splice form #status predicted <MATIF:27-169/Product: collagen alpha 5(IV) chain, leukocyte splice form #status F:41-462/Region: interrupted helical, NC2 #status predicted <NC2>
F:47-169/Promain: collagen IV carboxyl-terminal repeat <CT2>
F:143-153/Domain: collagen IV carboxyl-terminal repeat <CT2>
F:1482-1570, 1535-1537/Disulfide bonds: (or 1482-1573, 1515-1570) #status predicted F:1482-1570, 1515-1570) #status predicted F:1482-1570, 1515-1570) #status predicted F:1592-1684, 1626-1687/Disulfide bonds: (or 1592-1687, 1626-1684) #status predicted F:1592-1684, 1626-1688/Disulfide Bonds: (or 1592-1684, 1626-1684) #status predicted
collagen alpha 2(IV) chain precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999 C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999 C;Accession: A33526; A24432; D24432; A25066; B25066; A24364; S19081; B29301;
                                                                                                                                                      RESULT
A33526
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A;Residues: 1-754 <ZHE>
A;Cross-references: GB:U07888; NID:g469547; PIDN:AAB60258.1; PID:g469548
C;Superfamily: collagen alpha 1(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 5(IV) chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999
C:Accession: A55267
R:Zheng, K.; Thorner, P.S.; Marrano, P.; Baumal, R.; McInnes, R.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 3989-3993, 1994
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en type IV.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                         355 GIKGERGNPGQPGQP
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                                                                                                                                                                                                                                                                                                                                                                           1 GVKGDKGNPGWPGAP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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73.38;
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Pred. No. 0.038;
3; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-1707 <SAU>
A; Cross-references: EMBL: J04695; NID: g556298; PIDN: AAA50293.1;
R; Kurkinen, M.; Bernard, M.P.; Barlow, D.P.; Chow, L.T.
Nature 317, 177-179, 1985
                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1480-1572, L',1574-1622, H',1624-1707
A; Cross references: EMBL:X04647
R; Kaytes, P.; Wood, L.; Theriault, N.; Kurkinen, M
J. Biol. Chem. 263, 19274-19277, 1988
A; Title: Head-to-head arrangement of murine type I
A; Reference number: A92702; MUID:89066738
                                                                                                                                                                                                                                                                                                                                                                             A;Cross*references: EMBL:M15833; NID:g192284; PIDN:AAA37341.1; R;Schwarz-Magdolen, U.; Oberbaeumer, I.; Kuehn, K. R;Schwarz-Magdolen, U.; Oberbaeumer, I.; Kuehn, K. FEBS Lett. 208, 203-207, 186 A;Title: CDNA and protein sequence of the NC1 domain of the alp A;Reference number: A24628; MUID:87054581
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A; Molecule type: mRNA
A; Residues: 1466-1622, 'H', 1624-1707 <KA1>
A; Cross-references: GB: X04410; NID: g50240; PIDN: CAA27998.1; PID: g929678
A; Cross-references: GB: X04410; NID: g50240; Barlow, D.P.; Quinones, S.; Saus, J.; Pih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA, A; Molecule type: mRNA, A; Molecule type: mRNA, A; Residues: 1041-1050, R', 1052-1170, 'S', 1172-1178, 'R', 1180-1240, 'E', 1242-1327, 'A', 132 A; Cross-references: EMBL: X04410; NID: 950240; PIDN: CAA27998.1; PID: 9929678 R; Kaytes, P.S.; Theriault, N.Y.; Vogell, G. Gene 54, 141-146, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Saus, J.; Quinones, S.; MacKrell, A.; Blumberg, B.; Muthukumaran, J. Biol. Chem. 264, 6318-6324, 1989
A;Title: The complete primary structure of mouse alpha-2(IV) collage A;Reference number: A33526; MUID:89197933
A;Accession: A33526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kurkinen, M.; Condon, M.R.; Blumberg, B.; J. Biol. Chem. 262, 8496-8499, 1987 A;Title: Extensive homology between the carb A; Reference number: A94680; MUID:87250460 A;Accession: B29301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Homologies between the non-collagenous C-terminal (NC1) globular domains A;Reference number: S19080; MUID:87277427 A;Accession: S19081
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FEBS Lett. 206, 29-32, 1986
A;Title: Proposed alignment of helical interruptions in
A;Reference number: A24364; MUID:87005245
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Eur. J. Biochem. 157, 49-56, 1986
A;Tille: Structure of mouse type IV collagen.
A;Reference number: A25066; MUID:86220192
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A; Residues: 967-1096, 'G', 1098-1109 <KUl>
A; Cross-references: EMBL: X02896; NID: 950263;
A; Note: the authors translated the codon AAC
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A;Accession: A24432
                                                                A; Molecule type: DNA
A; Residues: 1-33 <KA2>
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A; Residues: 979-1058;1065-1101;1105-1222;1226-1310;1326-1335;1351-1480
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A; Residues: 964-1096, 'G', 1098-1109 < KU2>
                                                                                                                             A; Accession:
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A; Residues: 1481-1707 < KUR>
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A; Residues: 970-1480 <SC1>
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                           Cross-references: EMBL: J04448; NID: g192666;
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Martin,
G.R.;
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                                                                                                                                                                                                                                                   N.; Kurkinen, M.; Vogeli,
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for residue 964 a
                                 PIDN:AAA37438.1; PID:g192667
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                                                                                                                                                                                             IV collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the alpha-2-chain of collager
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A;Introns: 15/2; 33/3; 963/1; 1003/3; 1064/3; 1085/3
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: basement membrane; cell binding; coiled coil; dis
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1707/Product: collagen alpha 1(IV) chain #status predict
F;29-171/Domain: 75 #status predicted <75D>
F;29-171/Domain: 011agenous #status predicted <COL>
F;141-143/Region: cell attachment (R-G-D) motif
F;360-362/Region: cell attachment (R-G-D) motif
F;884-886/Region: cell attachment (R-G-D) motif
F;985-967/Region: cell attachment (R-G-D) motif
F;985-967/Region: cell attachment (R-G-D) motif
F;985-967/Region: cell attachment (R-G-D) motif
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A;Reference number: S19086
A;Accession: S19086
A;Molecule type: prot
A;Residues: 1475-1481
C;Genetics:
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F;884-886/Region: cell attachment (R-G-D) motif
F;965-967/Region: cell attachment (R-G-D) motif
F;965-967/Region: cell attachment (R-G-D) motif
F;123-1225/Region: cell attachment (R-G-D) motif
F;1247-1249/Region: cell attachment (R-G-D) motif
F;1481-159/Region: cell attachment (R-G-D) motif
F;1481-159/Domain: cepeat NC1 #status predicted <NC12>
F;1481-1589/Domain: repeat NC1 #status predicted <NC12>
F;1481-153,481,483/Disulfide bonds: interchain #status predicted
F;138,1270/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;138,1270/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;566-676,1544-1550,1653-1660/Disulfide bonds: #status predicted
F;985,988,997,1003,1028,1031,1067,1101,1113,1119,1143,1170,1200,1242,1305,1368,1391/Bind;F;985,988,997,1003,1028,1031,067,1101,1113,1119,1143,1170,1200,1242,1305,1368,1391/Modif;1009,1012,1018,1021,1024,1037,1040,1043,1046,1055,1058,1070,1098,1110,1128,1140,1149,177,1383,1386,1401,1408,1420,1423,1429,1444,1465,1468,1471,1477/Modified site: hydroxypro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1990 #text_change 22-Jun-1990 #text_change 22-Jun-1990 #text_change 22-Jun-1990 #text_change 22-Jun-1990 #text_change 22-
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R;Weber, S.; Engel, J.; Wiedemann, H.; Glanville, R.W.;
Eur. J. Blochem. 139, 401-410, 1984
A;Title: Subunit structure and assembly of the globular
A;Reference number: S17801; MUID:84132058
                                                                                       A:Reference number: S00007; MUID:87219158
A:Accession: S00007
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                                                                                                                                                                                                                                                                               R; Hostikka, S.L.; Kurkinen, FEBS Lett. 216, 281-286, 19
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                                                                                                                                                                                                                                    A; Title: Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-1712 < HOS1>
A; Cross-references: EMBL: J04210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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lecule type: mRNA
sidues: 1254-1398,'V',1400-1712
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nes: procollagen alpha 2(IV) chain
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66.7%;
                                                                                                                                                                                                                                                                                                                      M.; Tryggvason,
                                                                                                                                                                                                                                    coding for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB Pred. No. 0.12 2; Mismatches
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A;Note: the sequence from Fig. 4 is inconsistent R;Eble, J.A.; Golbik, R.; Mann, K.; Kuehn, K. RMBO J. 12, 4795-4802, 1993
A;Title: The alpha-1-beta-1 integrin recognition: A;Reference number: S39614; MUID:94038963
A;Accession: S39615
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R; Oberbaeumer, I.
submitted to the EMBL Data
submitted number: S17678
A; Molecule type: protein
A; Residues: 407-570 <EBL>
R: MacWright, R.S.; Benson, V.A.;
Biochemistry 22, 4940-4948, 1983
                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 37-247 <SIE1>
                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S00165; A; Accession: S00165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: this sequence was submitted to the EMBL Data Library, R;Siebold, B.; Qian, R.Q.; Glanville, R.W.; Hofmann, H.; Deut. Eur. J. Biochem. 168, 569-575, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-33 <SOI2>
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A; Residues: 1-33 <SOII>
A; Residues: 1-33 <SOII>
A; Cross-references: EMBL: J04217; EMBL: J05039; NID: g180759; PIDN: AAA53097.1;
A; Cross-references: EMBL: J04217; EMBL: J05039; NID: g180759; PIDN: AAA53097.1;
C; Soininen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K.
J. Biol. Chem. 264, 13565-13571, 1989
A; Title: Structural organization the gene for the alpha-1 chain of human A; Title: Structural organization the gene for the alpha-1 chain of human A; Reference number: $16876; MUID: 89340433
A; Accession: $16877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 263, 17217-17
A;Title: The structural gene
A;Reference number: A92690;
A;Accession: B32117
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A;Title: The structural genes for alphal and alpha2 chains of human type A;Reference number: A92690; MUID:89034231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-33 < POE>
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A; Residues: 1-470, 'p',472-682,'G',684-1043 <OBE>
A; Cross-references: EMBL: X05562; NID: 930075; PIDN: CAA29076.1;
R; Poeschl, E.; Pollner, R.; Kuehn, K.
EMBO J. 7, 2687-2695, 1988
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A; Residues: 1-682,'G', 684-1043 <BRA>
A; Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1;
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A; Residues: 1347-1350;1377-1383;1426-1432;1465-1471;1529-1535;1625-1630
A; Residues: ucleotide sequence not shown
A; Note: complete nucleotide sequence not shown
R; Brazel, D.; Pollner, R.; Oberbaeumer, I.; Kuehn, K.
Eur. J. Biochem. 172, 35-42, 1988
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A;Note: 1399-ILe was also found
R;Hostikka, S.L.; Tryggvason, K.
FEBS Lett. 224, 297-305, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Construction of a model for the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: J04217; NID: g180759; PIDN: AAA53097.1; PID: g553233;
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                              Lovello,
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                              K.T.; van der
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                                 Fietzek, P.P
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Isolation and characterization of nce number: S16910; MUID:84053346

pepsin-solubilized

human

basement membrane

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A; Molecule type: protein
A; Residues: 1480-1535; 1545-1614; 1617-1662, 'H', 1664-1700, 'G'; 1705-1708; 1710-1712
A; Residues: 1480-1535; 1545-1614; 1617-1662, 'H', 1664-1700, 'G'; 1705-1708; 1710-1712
A; Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in h
R; Myers, J.C.; Howard, P.S.; Jelen, A.M.; Dion, A.S.; Macarak, E.J.
J. Biol. Chem. 262, 9231-9238, 1987
A; Title: Duplication of type IV collagen COOH-terminal repeats and species-special; Reference number; A27114; MUID:87250571
A; Accession: B27114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:119792; OMIM:120090
A:Map position: 13934-13934
A;Introns: 15/2; 33/3; 1347/1; 1380/1; 1429/1; 1468/1; 1532/1; 1527/3 *status incomplete A;Introns: 15/2; 33/3; 1347/1; 1380/1; 1429/1; 1468/1; 1532/1; 1527/3 *status incomplete A;Note: the alpha 1(IV) and alpha 2(IV) chain genes are encoded on opposite strands with C;Complex: Type IV collagen is a heterotrimer of two alpha 1(IV) chains (see PIR:CGHU4B) domains (with disulfide and desmosine cross-links).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:J02760; NID:g180425; PIDN:AAA58422.1; PID:g180426 C;Comment: Prolines and lysines at the third position of the tripeptide repeating ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1486-1574, 'I', 1576-1712 <MYE>
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Eur. J. Biochem. 176, 617-624, 1988
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A; Residues: 1040,'L',1042-1398,'V',1400-1418,'M',1420-1635,'V'
A; Cross-references: EMBL:M24/66; NID:g537328; PIDN:AAA52043.1;
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A;Reference number: $22243
A;Reference number: $23296
A;Accession: $23296
A;Status: not compared with conceptual transl A;Status: not compared with conceptual transl A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-677 <NII>
R;Nishimura, I; Muragaki, Y; Olsen, B.R.
J, Biol. Chem. 264, 20033-20041, 1989
A;Title: Tissue-specific forms of type IX co
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C;Accession: S2396; C34493; A290
R;Ninomiya, Y; Castagnola, P;
maguchi, N; Olsen, B.R.
in Extracellular Matrix Genes, Sc
A;Title: The molecular biology of
                                                                                                                                                                                                                                                                 R:Lozano, G.; Ninomiya, Y.; Thompson, H.; Olsen, B.R. Proc. Natl. Acad. Sci. U.S.A. 82, 4050-4054, 1985 A;Title: A distinct class of vertebrate collagen genes A; Reference number: A94705; MUID:85216631 A; Accession: B28754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M16715; NID:9211365; PA;Accession: B29032
A;Mclecule type: protein
A;Residues: 147-165;170-180,'X',182-188 <MC2>
R;Lozano, G.; Olsen, B.R.
submitted to the EMBL Data Library, April 199; A;Reference number: S22062
A;Accession: S22062
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A;Accession: C34493
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-174 <NIS>
A;Cross-references: EMBL:M28660; NID:g211625; PIDN:AAA48709.1; PID:g211626
R;MCCormick, D.; van der Rest, M.; Goodship, J.; Lozano, G.; Ninomiya, Y.;
Proc. Natl. Acad. Sci. U.S.A. 84, 4044-4048, 1987
A;Title: Structure of the glycosaminoglycan domain in the type IX collagen-A;Reference number: A29032; MUID:87231947
A;Accession: A29032
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A;Title: Construction and characterization A;Reference number: A18856; MUID:86026268 A;Accession: A18856 A;Molecule type: mRNA
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 404-633; 644-677 <LO2>
A; Cross-references: EMBL:M11327
                                                                                                          Biochemistry 24, 4223-4229, 1985
                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 401,'RA',404-631,'D',633-677 <LO1>
A;Cross-references: EMBL:M11327
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A; Residues: 120-195 <
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sion: S23296; C34493; A29032; B29032; S22062; B28754; A18856; B18856; A28518;
iya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.;
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                                                                                                                                                         sequence has been revised in
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lus gallus (chicken)
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GB:M16715; NID:g211365; PIDN:AAA48644.1;
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                                                                              cDNA encoding the alpha2 chain
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Ann. N. Y. Acad. Sci. 460, 38-46, 1985
A; Title: The structure of type IX collagen.
A; Reference number: $22238; MUID:86185164
A; Accession: $22239
A; MOlecule type: protein
A; Residues: 542-567 < MAY>
C; Genetics:
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C;Superfamily: unassigned collagens
C;Superfamily: unassigned collagens
C;Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycopi
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-677/Product: collagen alpha 2(XI) chain #status predicted <MAT>
F;23-161/Domain: collagenous COL3 #status predicted <NC3>
F;162-178/Domain: non-collagenous NC3 #status predicted <NC3>
F;179-517/Domain: collagenous COL2 #status predicted <NC2>
F;518-547/Domain: non-collagenous NC3 #status predicted <NC2>
F;518-547/Domain: non-collagenous NC2 #status predicted <NC1>
F;563-677/Domain: non-collagenous NC1 #status predicted <NC1>
F;663-677/Domain: non-collagenous NC1 #status predicted <NC1>
F;663-677/Domain: non-collagenous NC1 #status predicted <NC1>
F;158,178/Modified site: 4-hydroxyproline (Pro) #status experimental
F;167/Binding site: Chondroltin sulfate (Ser) (covalent) #status experimental
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A; Residues: 433-435,'X', 437-450;542-562 <NI3>
A; Residues: 5: Winterhalter, K.H.; Vaughan, L.
J. Biol. Chem. 263, 752-756, 1988
A; Title: Isolation and sequence analysis of the glycosaminoglycan attachment site of type A; Reference number: A28518; MUID:88087195
A; Accession: A28518
                                                                                                                                                                                                                                                               C;Accession: A54849; PHÓ844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alphal(VIA); Reference number: A54849; MUID:94327588
                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: procollagen alpua 1(v11) cm....
C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change
                                           Biochem.
                                                                                                                                                                                                                                     A; Reference number: A54849; A; Accession: A54849
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A;Accession: S23813
                                                                            R;Tanaka,
                                                                                                      A;Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
                                                                                                                                           A; Residues: 1-2944 <CHR>
                                                                                                                                                                  A; Molecule type: mRNA
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A; Residues: 170-180, 'X', 182-184 <VAN>
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J. Biol. Chem.
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Residues: 156-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Modified site: 5-hydroxylysine (Lys) #status experimental /Binding site: carbohydrate (Lys) (covalent) #status experimental //Modified site: allysine (Lys) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GVKGDKGNPGWPGAP 15
, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biophys. Res. Commun. 183, 958-963, 1992
Molecular cloning and characterization of type VII collagen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIDGDKGSPGAPGSP
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156-159,'x',161-166,'X',168-173,'X',175-178 <нUB>
est, M.; Mayne, R.
em. 263, 1615-1618, 1988
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                                                                                                                                                                                                    conceptual translation
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Pred. No.
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0.094;
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                                                                                                                          F:36-201/Domain: von Willebrand fac
F:231-318/Domain: fibronectin type
F:327-413/Domain: fibronectin type
F:414-502/Domain: fibronectin type
F:508-593/Domain: fibronectin type
F:598-683/Domain: fibronectin type
                                       F;776-862/Domain:
F;864-952/Domain:
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A; Molecule type: mRNA
A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A; Cross references: GB: S51236; NID: g262308; PIDN: AAB24637.1; PID: g262309
A; Cross references: GB: S51236; NID: g262308; PIDN: AAB24637.1; PID: g262309
R; S61tzer, J.L., Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; l
J. Biol. Chem. 264, 3822-3826, 1989
A; Title: Cleavage of type VII collagen by interstitial collagenase and type
A; Reference number: A30296; MUID: 89139437
A; Rocession: A30296
A; Molecule type: protein
A; Rosidues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E'; 2032,''
A; Rosidues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E'; 2032,''
A; Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: unassigned collagens; animal Kunitz-type proteinase in C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxyly. F;17-16/Domain: signal sequence #status predicted <SIG> F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: there are 118 introns
C; Complex: type VII collagen is probably a homotrimer
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A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser s A;Reference number: A55255; MUID:94224777 A;Contents: annotation C;Comment: Prolines and lysines at the third position of the tripeptide repeating uniced and services and the services and the services and the services are services as the services are services and the services are services as the services a
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 2395-2871,'S',2873-2944 <RE2>
A;Cross references: GB:U06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type
A; Reference number: 148103; MUID:93271985
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A;Title: Noncollagenous (NC1) domain of collagen
A;Reference number: I56328; MUID:93107742
A;Accession: I56328
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A;Molecule type: mRNA
A;Residues: 'EFK', '340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG', '524-528,'
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g4536
A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.;
PTOC. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA coloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380
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A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Cross-references: GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96439.1; PID:g180915
A; Experimental source: keratinocyte
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1253/Domain: amino-terminal nonhelical #status predicted 201/Domain: von Willebrand factor type A repeat homology <1318/Domain: fibronectin type III repeat homology <FN1>
-413/Domain: fibronectin type III repeat homology <FN2>
-502/Domain: fibronectin type III repeat homology <FN3>
-593/Domain: fibronectin type III repeat homology <FN4>
-683/Domain: fibronectin type III repeat homology <FN5>
-771/Domain: fibronectin type III repeat homology <FN5>
-862/Domain: fibronectin type III repeat homology <FN7>
-952/Domain: fibronectin type III repeat homology <FN7>
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Willebrand

factor

Þ homology

homology <VWA2>

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A; Molecule type: mRNA
A; Residues: 1-1414 < EXP>
A; Residues: 1-1414 < EXP>
A; Cross-references: EMBL: M92040; NID: g161435; PIDN: AAA30035.1; PID: g161436
A; Cross-references: EMBL: M92040; NID: g161435; PIDN: AAA30035.1; PID: g161436
C; Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal c; Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple F; 1207-1414/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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F:1189-1253/Region: cystcine/prolinerrich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif
F:1038-2010/Region: cell attachment (R-G-D) motif
F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2553/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F:287-6-2949/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F:287-6-2949/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F:287-6-2949/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F:287-6-294/Domain: animal Kunitz-type proteinase inhibitor homology <BPI
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R;Saltta, B.; Buttice, G.; Gambino, R.
R;Saltta, B.; Buttice, G.; Gambino, R.
Biochem. Biophys. Res. Commun. 158, 633-639, 1989
A;Title: Isolation of a putative collagen-like gene
A;Reference number: A32249; MUID:89149773
A;Accession: A32249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Exposito, J.Y.; d'Alessio, M.; Solursh, M.; Ramirez, F.
J. Blol. Chem. 267, 1559-15562, 1992
A;Title: Sea urchin collagen evolutionarily homologous to vertebrate pro-alpha-2(I) col A;Reference number: S23809; MUID:92348411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Strongylocentrotus purpuratus (purple urchin) (;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text C;Accession: S23809 R;Exposito, J.Y.; d'Alessio, M.; Solursh, M.; Ramirez, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 2(I) chain homolog - sea urchin (Strongylocentrotus purpuratus)
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C;Species: Paracentrotus lividus (common urchin)
C;Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 19-Jan-1996
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   Query Match
Best Local
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Best Local
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   Local Similarity
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12; Conserv
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Pred. No. 0.41;
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N 62;
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0.28;
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A; Molecule type: mRNA, A; 7.595-1670 < MOR>
A; Residues: 1453-1593, A', 1595-1670 < MOR>
A; Cross-references: GB:S55790; NID:g234418; PIDN:AAB19637.1; C; Comment: Prolines and lysines at the third position of the ed and subsequently O-glycosylated.
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A;Title: Sequence and localization of a partial cDNA encoding A;Reference number: A39786; MUID:91353570
A;Accession: A39786
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A;Title: Molecular cloning of the human Goodpasture antigen demonstrates A;Reference number: A43928; MUID:92147878
A;Accession: A43928
A;Map position: 2q36-2q37
A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite C;Complex: This minor type IV collagen is thought to form a heterotrimer of
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A;Residues: 1386-1670 <QUI>
A;Residues: 1386-1670 <QUI>
A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
R;Quinones, S.; Bernal, D.; Garcla-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: kidney
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus,
J. Biol. Chem. 267, 19780-19784, 1992
A;Title: Exon/intron structure of the human alpha 3(IV) gene en
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A;Title: Complete primary structure of the human alpha3(IV)
A;Reference number: A54763; MUID:94364994
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C;Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999 C;Accession: A54763; A43928; A44043; A45971; A39786
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A; Residues: 1331-1524, 'I', 1526-1670 <TUR>
A; Cross-references: GB: M81379
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A;Residues: 1-1670 <MAR>
A;Cross-references: GB:X80031; NID:9577563; PID:9577564
A;Experimental source: kidney
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                                                                                                                                                  A;Cross-references: GDB:128351; OMIM:120070
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A; Residues: 1427-1444 <BER>
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                                                                                   1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
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C:Reywords: alternative splicing; basement membrane; cell binding; coiled coil; extracel F:1-28/Domain: signal sequence #status predicted <SIG>F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>F:29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MAT>F:29-1670/Product: collagen incorrent (R-G-D) motif F:43-1438/Region: cell attachment (R-G-D) motif F:191-793/Region: cell attachment (R-G-D) motif F:1306-1308/Region: cell attachment (R-G-D) motif F:1345-1347/Region: cell attachment (R-G-D) motif F:1432-1434/Region: cell attachment (R-G-D) motif F:1432-1434/Region: cell attachment (R-G-D) motif F:1431-1551/Domain: cell attachment (R-G-D) motif F:1431-1551/Domain: cell attachment (R-G-D) motif F:1431-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>F:1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT1>F:1511-1551/Domain: collagen IV carboxyl-terminal repeat <CT2>F:1511-1551/Disulfide bonds: (corlagent) #status predicted F:1460-1548,1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted F:1505-1511,1616-1622/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted F:1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted F:1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted F:1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted
collagen alpha 1(XVI) chain precursor - human N;Alternate names: procollagen alpha 1(XVI) chain C:Species: Homo sapiens (man)
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A; Description: minor structural component of extracellular basement membrane in C; Superfamily: collagen alpha 1(IV) chain C; Keywords: alternative splicing; basement membrane; cell binding; coiled coil; F; 1-28/Domain: signal sequence #status predicted <SIG>
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A;Title: Capsomer proteins of bacteriophage
A;Reference number: A46345; MUID:90320115
A;Accession: B46345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: phage PRD1
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
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A;Accession: D46345
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A; Residues: 1-340 <BAM>
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R; Bamford, J.K.H.; Bamford, D.H.
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;Reywords: capsid protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ng trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a associations in the interrupted helical domain (with disulfide and desmosine cross-li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V protein - phage PRD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1189 GAKGDRGAPGFPGLP 1203
                                                                                                                                                                                                                                   124 GIKGDKGDPGAPG
                                                                                                                                                                                                                                                                                                                                                             / Match 66.3%;
Local Similarity 76.9%;
nes 10; Conservative
                                                                                                                                       14
                                                                                                                                                                                                                                                                                              1 GVKGDKGNPGWPG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GVKGDKGNPGWPGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : protein

<BA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              minor capsid protein V
                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g215745; PIDN:AAA32446.1; PID:g215746
                                                                                                                                                                                                                                                                                                                                                      Score 61;
Pred. No. 1
2; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB
Pred. No. 0.33
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRD1, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                           .094;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kidney
   collagen alpha 4(IV)
                                       ССНО1В
                                                                                                                                                                    Дb
                                                                     RESULT
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F;334-360/Domain: collagenous COLIO #status predicted <CO10>
F;375-505/Domain: collagenous COLIO #status predicted <COLIO+
F;521-554/Domain: collagenous COLB #status predicted <COLB>
F;521-554/Domain: collagenous COLB #status predicted <COLB>
F;529-541/Region: cell attachment (R-G-D) motif
F;572-630/Domain: collagenous COLF #status predicted <COLF>
F;652-722/Domain: collagenous COLF #status predicted <COLF>
F;652-722/Domain: collagenous COLF #status predicted <COLF>
F;738-875/Domain: collagenous COLF #status predicted <COLF>
F;887-938/Domain: collagenous COLF #status predicted <COLF>
F;973-987/Domain: collagenous COLF #status predicted <COLF>
F;1005-1007/Region: cell attachment (R-G-D) motif
F;1011-1432/Domain: collagenous COLF #status predicted <COLF>
F;1276-12577/Domain: collagenous COLF #status predicted <COLF>
F;1578-1603/Domain: collagenous COLF #status predicted <COLF>
F;1578-1603/Domain: collagenous COLF #status predicted <COLF>
F;1578-1603/Domain: collagenous COLF #status predicted <COLF>
F;47,327/Binding site: carbohydrate (Asn) (covalent) #status predicted <NCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kimura, ;
submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-21/Domain: signal sequence #status predicted <SIG>F;22-1603/Product: collagen alpha 1(XVI) chain #status predicted <MAT>F;22-134)Comain: amino-terminal nonhelical #status predicted <NC11>F;334-1577/Region: interrupted helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: structural component of extracellular fibrous polymer as a minor form A; Note: may play a role in forming elastic connections at fibril surfaces C; Superfamily: unassigned collagens C; Keywords: cell binding; coiled coil; extracellular matrix; glycoprotein; hydroxylys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:COL16A1
A;Cross references: GDB:134045; OMIM:120326
A;Map position: 1p34-1p34
C;Complex: type XVI collagen may be a homotrimer, or a heterotrimer of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA A; Residues: 403-419, 'GR', 421-536, 'P', 538-846, 'VN' <KIM>A; Residues: 403-419, 'GR', 421-536, 'P', 538-846, 'VN' <KIM>A; Cross-references: EMBL:X14963; NID:g29984; PIDN:CAA33085.1; C:Comment: Prolines and lysines at the third position of the eed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S08012
A; Accession: S08012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, April 1989 A; Description: Partial nucleotide and amino ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Molecular cloning and partial characterization of a novel collagen chain, al A;Reference number: PQ0612; MUID:93203161
A;Accession: PQ0612
A;Molecule type: mRNA
A;Residues: 'GGR',421-536,'P',538-1159,'P',1161-1162,'P',1164,'P',1166-1603 <YAM>
A;Cross-references: GB:S57132; NID:9298641; PIDN:AAB25797.1; PID:9298642
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A; Cross-references: EMBL: M92642; NID: g180757; PIDN: AAA58427.1; PID: g180758
A; Experimental source: skin fibroblasts
R; Yamaguchi, N.; Kimura, S.; McBride, O.W.; Hori, H.; Yamada, Y.; Kanamori
J. Biochem. 112, 856-863, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 20-Sep-1 C;Accession: S23810; PQ0612; S08012 R;Pan, T.C.; Zhang, R.Z.; Mattei, M.G.; Timpl, R.; Chu, M.L. Proc. Natl. Acad. Sci. U.S.A. 89, 6565-6569, 1992 A;Title: Cloning and chromosomal location of human alpha1(XVI) collagen. A;Reference number: S23810; MUID:92335339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S23810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                        Matches
    681 GQKGDAGNPGDPGTP
                                                                                                                                                                                        Local Similarity
                                                                            1 GVKGDKGNPGWPGAP 15
                                                                                                                                                        Conservative
                                                                                                                                                                                        66.3%;
699
                                                                                                                                                    Score 61; DB
Pred. No. 0.44
0; Mismatches
                                                                                                                                                                                        DB 2;
0.44;
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                                                                                                                                                                                                                         Length 1603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PID:g930048
tripeptide r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen-like protein
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                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                          <NC01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha 1(XV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.; Yamak
                                                                                                                                                        0;
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chain

precursor

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J. Biol. Chem. 269, 26172-26177, 1994
A;Title: Complete primary structure of the human type IV collagen alpha4(IV)
A;Reference number: A55360; MUID:95014445
A;Status. 7...75360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-1690/product: collagen alpha 4(IV) chain #status predicted <MAT>
F;39-61/Domain: amino-terminal nonhelical, NH1 <NH1>
F;39-61/Domain: interrupted helical
F;94-96/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                er associations in the interrupted helical domain (with disulfide and desmosine cross-: C; Function:
A; Description: minor structural component of extracellular basement membrane in kidney C; Superfamily: collagen alpha 1(IV) chain
C; Keywords: basement membrane; coiled coil; extracellular matrix; glycoprotein; hydrox; F; 1-38/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Introns: 39/1; 1406/1; 1445/1; 1508/1; 1603/3 *status incomplete A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands with C:Complex: this minor type IV collagen is thought to form a heterotrimer of two alpha 3 mong trimer aminor-terminal domains (with disulfide and desmosine cross-links), dimeric er associations in the interrupted helical domain (with disulfide and desmosine cross-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1690 < LEI>
A; Cross-references: GB: X81053; NID: 9574805; PIDN: CAA56943.1; PID: 9574806
A; Cross-references: GB: X81053; NID: 9574805; PIDN: CAA56943.1; PID: 9574806
A; Cross-references: GB: X81053; NID: 9574805; PIDN: CAA56943.1; PID: 9574806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:145-147/Region: cell attachment (R-G-D) motif F:189-91/Region: cell attachment (R-G-D) motif F:310-312/Region: cell attachment (R-G-D) motif F:724-726/Region: cell attachment (R-G-D) motif F:785-787/Region: cell attachment (R-G-D) motif F:785-787/Region: cell attachment (R-G-D) motif F:989-991/Region: cell attachment (R-G-D) motif F:921-7214/Region: cell attachment (R-G-D) motif F:921-7214/Region: cell attachment (R-G-D) motif F:921-7214/Region: cell attachment (R-G-D) motif
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A; Residues: 1407-1424, 'G', 1426-1430, 'A', 1432-1439, 'L', 1441-1507 <KANN>
A; Residues: 1607-1475; GB:L01476
A; Cross-references: GB:L01475; GB:L01476
A; Note: the codons given for 1438-Asp (GAG) and 1443-Gly (GCA) are inconsistent C; Comment: Prolines and lysines at the third position of the tripeptide repeatin ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: whole eye R:Kamagata, Y.; Mattel, M.G.; Ninomiya, Y. J. Biol. Chem. 267, 23753-23758, 1992 A:Title: Isolation and sequencing of cDNAs and A:Reference number: $28777; MUID:93054733 A:Accession: $28777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: cDNA isolation and partial gene structure of A;Reference number: S36854; MUID:93374047 A;Accession: S36854
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:132673; OMIM:120131
A;Map position: 2q35-2q37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA; mRNA
A;Residues: 1219-1658,'FE',1661-1690 <SUG>
A;Cross-references: DDBJ:D17391; NID:g440365;
                                                                                                                                                                                                                                                                                                                                                                                       :1467-1690/Domain: carboxyl-terminal nonhelical, NC1 <NC1>
:1471-1569/Domain: collagen IV carboxyl-terminal repeat <CT1>
:1579-1686/Domain: collagen IV carboxyl-terminal repeat <CT2>
:47,52,55,57,266,400,460,492,494,668,790,828,1095,1131,1294,1317,1375,1407/Disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternate names: procollagen alpha 4(IV) chain
                                                                                                                                                                                                                                                142,669/Binding site: carbohydrate (Asn) (covalent) #status predicted 1400-1566,1513-1569/Disulfide bonds: (or 1480-1569, 1513-1566) #status 1525-1531,1634-1641/Disulfide bonds: #status predicted 1525-1531,1634-1641/Disulfide bonds: #status predicted 1588-1683,1622-1686/Disulfide bonds: (or 1588-1686, 1622-1683) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: GDB:COL4A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence not shown
                                                                                                            66.3%;
                                                                           Score 61; DB
Pred. No. 0.4(
4; Mismatches
                                                                                                                0.46;
                                                                                                                                          ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN: BAA04214.1;
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                                                                                                                                          ۲,
                                                                           <u>ب</u>
                                                                                                                                              Length 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the human alpha-4(IV) collagen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding the alpha4
                                                                           0
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                           predicted
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F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-1763/Product: collagen alpha 2(IV) chain #status predicted
F:27-42/Domain: non-collagenous NH1 #status predicted <NH1>
F:43-1529/Domain: collagenous #status predicted <COL>
F:197-199/Region: cell attachment (R:G-D) motif
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A,Title: The complete primary structure of A-Reference number: S16366; MUID:91340768
                                                                                                                                                                                                                                                                                                                                                                C;ACCe8810n: 1997
R;Nah, H.D.; Niu, Z.; Adams, S.L.
J. Biol. Chem. 269, 16443-16448, 1994
A;Title: An alternative transcript of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1530-1763/Domain: carboxyl-terminal nonhelical, NCl #status predicted F;1530-1648/Domain: repeat NCl #status predicted <NCll>F;1530-1658/Domain: repeat NCl #status predicted <NCll>F;1639-1763/Domain: repeat NCl #status predicted <NCll>F;31,34,39,41,536,539/Disulfide bonds: interchain #status predicted F;126/Binding site: carbohydrate (Asn) (covalent) #status predicted F;1593-1599,1702-1709/Disulfide bonds: #status predicted
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C;Species: Ascaris suum (pig roundworm)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-310 <NAH>
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C;Keywords: alternative splicing; basement membrane;
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A; Residues: 1-1763 <JBI>
A; Cross-references: GB:M
                                                                                                                                                                     A;Gene: COL3A1
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 1(III) chain - chicken (fragment)
C; Species: Gallus gallus (chicken)
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1 GVKGDKGNPGWPGA 14
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lly: collagen alpha 1(IV) chain
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10; Conserv
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266, 16149-16156, 1991
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73.3%;
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                                                                       Score 60; DB 2
Pred. No. 0.12;
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Pred. No. 0.48;
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281 GVKGERGSPGGPGA

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C;Species: Rattus norvegicus (Norway rat)
C;Bate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: $41067; A29905; $31924
R;Glumoff, V; Maekelae, J.K.; Vuorio, E.
Biochim. Biophys. Acta 1217, 41-48, 1994
A;Title: Cloning of cDNA for rat pro alpha-1(III) collagen mRNA. Different A;Reference number: $41067; MUID:94114571
A;Accession: $41067
                                                                                                                                                                                                        A;Molecule type: mRNA
A;Rosidues: 2-636 <GL2>
A;Cross-references: EMBL:X70369
A;Cross-references: EMBL:X70369
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: colled coll; extracellular matrix; glycoprotein; trimer; triple helix
F;408-636/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 308-482 <FRA>
A;Cross-references: GB:M21354; NID:g203500; PIDN:AAA40942.1; PID:g203501
R;Glumoff, V.; Maekelae, J.K.; Vuorio, E.
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: basement membrane
A; Note: sequence extracted from NCBI backbone (NCBIP:118549)
C; Superfamily: collagen alpha 1(IV) chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X70369; NID:g57915; PIDN:CAA49832.1; PID:g57916 R;Frankel, F.R.; Hsu, C.Y.J.; Myers, J.C.; Lin, E.; Lyttle, C.R.; Komm, IDNA 7, 347-354, 1988
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A; Accession: S31924
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A; Residues: 1-623 <KAM>
                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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GVKGERGSPGGPGA 43
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Pred. No. 0.25
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1; Mismatches
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0.25;
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A;Accessium: A;Accessium: A;Molecule type: protein
A;Molecule type: protein
A;Residues: 572-808 cLAN>
A;Residues: 572-808 cLAN>
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
R;Dewes, H.; Fietzek, P.P.; Fietzek, R.
R;Dewes, H.; Fietzek, P.P.; Fietzek, R.
R;Dewes, H.; Fietzek, P.P.; Fietzek, R.
R;Dewes, H.; F
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 423-571 <BEN>
A; Residues: 423-571 <BEN>
A; Residues: 423-571 <BEN>
A; Residues: 423-571 <BEN>
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
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R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
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R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Fietzek, P.P.; Kuehn, K.
R; Lang, H.; Glanville, R.W.; Fietzek, P.P.; Fiet
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Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III collagen. III. The amino acid
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A;Accession: A38001
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A; Residues: 1-242 < FIED:
R; Dewes, H.; Fietzek, P.P.; Kuehn, K.
R; Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832,
A; Title: The covalent structure of calf skin ty
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J. Biol. Chem. 269, 16443-16448, 1994
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Fietzek, P.P.;
Z. Physiol. Ch
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P.; Glanville, R.W.; Chem. 360, 861-868,
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Blockmen. J. 318, 497-503, 1996
A:Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A:Reference number: $71946; MUID:96404897
A:Reference number: $71946
A:Reference number: $71946
A:Reference number: $71946
A:Reference number: $71946
A:Residues: 87-106;1017-1029;1037-1049 <HEN>
A:Residues: 87-106;1017-1029;1037-1049 <HEN>
C:Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h C:Comment: The type III collagen molecule is a triner of identical chains, linked to ead C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C:Reywords: collagen alpha 1(III) chain #status experimental <CAB>
F:1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
F:1-104/Region: maino-terminal nonhelical telopeptide
F:55-104/Region: cell attachment (R-G-D) motif
F:95-754/Region: cell attachment (R-G-D) motif
F:975-978/Region: cell attachment (R-G-D) motif
F:935-937/Region: cell attachment (R-G-D) motif
F:935-937/Region: cell attachment (R-G-D) motif
F:1041-1049/Region: cell attachment (R-G-D) motif
F:107,950/modified site: allysine (Lys) #status experimental
F:107,950/modified site: allysine (Lys) #status predicted
F:107/Binding site: carboxyl-terminal nonhelical telopeptide
F:107,050/modified site: allysine (Lys) #status predicted
F:107,050/modified site: allysine (Lys) #status predicted
A; Molecule type: mRNA
A; Residues: 1-1196 <ALA>
A; Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA3
A; Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA3
A; Note: the complete sequence is not shown
R; Benson-Chanda, V; Su, M.W.; Well, D.; Chu, M.L.; Ra
Gene 78, 255-265, 1989
A; Title: Cloning and analysis of the 5' portion of the
A; Reference number: PE0011; MUID:89378752
A; Accession: PE0011
A; Molecule type: DNA
A; Residues: 1-176 <BEN>
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A;Molecule type: mRNA
A;Rosiduse: 1-1240, 'V',1242-1466 <PRC>
A;Rosiduse: 1-1240, 'V',1242-1466 <PRC>
A;Cross·references: EMBL:X14420; NID:g30057; PID:A;Cross·references: EMBL:X14420; NID:g30057; PID:A;Cross·references: EMBL:X14420; NID:g30057; PID:A;Cross·references: EMBL:X14420; NID:g30057; PID:A;Cross·references: EMBL:X1420; NID:G30057; PID:A;Cross·
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A:Accession: A38005
A:Molecule type: protein A;Residues: 948-1049 <ALL>A;Experimental source: skin R;Henkel, M.
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Best Local S
Matches 10
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;Species: 4-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000;

Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000;

-arresaion: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868
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3; Mismatches
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T.; Kuivaniemi, H
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A;Residues: 3,, ..., A;Experimental source: liver A;Experimental source: liver R:Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, J. Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5 of a splingly spring a splingly spring a splingly spring spring
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Biochemistry 17, 3404-3411, 1978
A;Title: Covalent structure of collagen: amin A;Reference number: A90414; MUID:79000343
A;Accession: A90414
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Biochem. J. 311, 939-943, 1993
A;Title: Abnormal type III collagen produced
A;Title: Abnormal type III collagen produced
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A; Molecule type: mRNA
A; Residues: 149-163, (°g', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-6
A; Residues: 149-163, (°g', 164-240, 'D', 229545; PIDN:CAA33387.1; PID:g930045
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleot R; Seyer, J.M.; Kang, A.H.
Biochemistry 16, 1158-1164, 1977
A; Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide pept A; Reference number: A90399; MUID:77134724
A; Accession: A90399; MUID:77134724
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A;Note: the authors translated th
R;Janeczko, R.A.; Ramirez, F.
Nucleic Acids Res. 17, 6742, 1989
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A;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398
A;Experimental source: liver
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A; Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398
A; Experimental source: liver
A; Note: sequence corrected by A94562; attachment of 2-0-
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A; Residues: 537-605
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A; Residues: 399-675,'N', 677-727 <SEY3>
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A; Residues: 1-170 < TOM>
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A; Residues: 302-423 <CHI>
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A; Residues: 186-194 <MIL>
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;Seyer, J.M.; M
lochemistry 19,
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        Mainardi, C.; Kang,
9, 1583-1589, 1980
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1161-1200 <MIS>
A; Cross-references: GB: M13146; NID: g180415; PIDN: AAA52003.1;
R: Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes
A; Reference number: 159025; MUID: 85216505
A; Accession: 179359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of A;Reference number: A93551; MUID:85087944
A;Accession: A93551
C; Genetics:
A; Gene: GDE
                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795;
A;Experimental source: 11
                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 260, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding A;Reference number: A92516; MUID:85157600
A;Accession: A92516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.;
Biochemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is
A;Reference number: I52393; MUID:86187804
A;Accession: I52393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1065-1155, 'P',1157-1466 <LOI>
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
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A; Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157
A; Experimental source: liver
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A;Accession: A90446
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A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1;
R;Seyer, J.M.; Kang, A.H.
R;Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
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A;Title: Human pro alphal(III) collagen: cDNA sequence for the 3'A;Reference number: S02119; MUID:88189827
A;Reference number: S02119; MUID:88189827
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J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3Al gene causes exon skipping
A;Reference number: A38303; MUID:91009133
A;Accession: A38303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Covalent structure of collagen: amino acid sequence A;Reference number: A90438; MUID:80198282
A;Accession: A90438
                                                                                                                                                                                 A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1165-1196 <EMA>
                                                            3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status:
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                                                                                                                                                                              the authors translated the codon TTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    human
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Ramirez, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 1(XVII) chain - human (fragment)
W.Alternate names: bullous pemphigoid 180K autoantig
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence_revision 12-Jul-1996 #
C;Accession: I56325; I55345; A61262
R;Gludice, G.J.; Emery, D.J.; Dlaz, L.A.
J. Invest. Dermatol. 99, 243-250, 1992
A;Title: Cloning and primary structural analysis of
A;Reference number: I56325; MUID:92381323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;161,1212/Modified site: allysine (Lys) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;548-1949/Modified site: 5-hydroxylysine (Lys) partial) #status experimental
F;548-949/Cleavage site: Gly-Ile (collagenase) #status experimental
F;548-949/Cleavage site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                         R.Giudice, G.J.; Squiquera, H.L.; Elias, P.M.; I
J. Clin. Invest. 87, 734-738, 1991
A;Title: Identification of two collagen domains
A;Reference number: A61262; MUID:91123476
A;Accession: A61262
                                                                                                                                                                                                                                                  A; Diacus. Processing in RNA
A; Molecule type: mRNA
A; Residues: 543-890, 'p' <RE2>
A; Cross references: GB: M63730; NID: g179520; PIDN: AAA51839.1;
A; Cross references: GB: M63730; Lias, P.M.; Diaz, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M91669; NID:g179516; PIDN:AAA35605.1; R;Li, K.H.; Sawamura, D.; Giudice, G.J.; Diaz, L.A.; Mattei, J. Biol. Chem. 266, 24064-24069, 1991
A;Title: Genomic organization of collagenous domains and chroa;Reference number: I55345; MUID:92084712
A;Accession: I55345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: structural component of extracellular fibrous polymer that maintains in C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo C;Reywords: colled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; F;1-23/Domain: signal sequence #status predicted <SIG> F;24-153/Domain: amino-terminal propeptide #status predicted <PRO> F;31-91/Domain: von Willebrand factor type C repeat homology <VWC> F;154-1221/Product: collagen alpha 1(III) chain #status predicted <MAT> F;154-167/Region: amino-terminal nonhelical telopeptide
                          A; Molecule type: mRNA
A; Residues: 543-890, 'P'
C; Genetics:
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A;Map position: 2q31-2q31

A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 141

A;Introns: the list of introns is incomplete; defects in this gene can result in Ehlers-C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfider of their length, is formed with desmosine cross-links made from lysine and allysin
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated
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A; Residues: 1-1532 < RES>
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F;1091-1093/Region: cell attachment (R-G-D) motif
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78.6%;
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autoantigen BPAG2; bullous pemphigoid

#text_change 21-Jul-2000

the

Bullous

pemphigoid autoantige

chromosomal assignment of hu

PID:g179517

Chu, M.L.; Uitto,

within the

bullous pemphigoid

autoant

PID:g179521

DB 1; 0.57;

Length 1466

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A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Molecule type: nucleic acid
A:Residues: 1-1752 <EXP>
A:Note: sequence extracted from NCBI backbone (NCBIP:126841)
A:Residues: 1.48, 261-272, 1991
A:Title: Primary mesenchyme cells of the sea urchin embryo require an autonomously produ
A:Reference number: A43903; MUID:92038439
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'P',633-1537,'G' <WES>
A:Residues: 'P',633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 3(IV) chain - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 22-Sep-1993 *sequence_revision 18-Nov-1994 *text_change 13-Aug-1999
C;Accession: A45407; A43903; A23940
R;Exposito, J.Y.; D'Alessio, M.; Di Liberto, M.; Ramirez, F.
J. Biol. Chem. 268, 5249-5254, 1993
A;Title: Complete primary structure of a sea urchin type IV collagen alpha chain and A;Reference number: A45407; MUID: 33186842
A;Accession: A45407
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C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13990
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A;Cross-references: FlyBase:FBgn0016075
C;Superfamily: collagen alpha l(IV) chain
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A:Description: Viking: identification and characterization of a novel type IV A;Reference number: Z17845
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A;Map position: 10q24.3-10q24.3
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Residues: 1-1761 <YAS>
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Pred. No. 0.68;
2; Mismatches
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A;Cross references: EMBL:M13206
C;Superfamily: collagen alpha 1(IV) chain
C;Keywords: colled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;29-161/Domain: amino-terminal nonhelical, 7S <7SD>
F;162-1523/Region: interrupted helical
F;1524-1752/Domain: carboxyl-terminal nonhelical, NCl <NCl>
F;1534-163/Domain: collagen IV carboxyl-terminal repeat <CTl>
F;1534-163/Domain: collagen IV carboxyl-terminal repeat <CTl>
F;1644-1748/Domain: collagen IV carboxyl-terminal repeat <CTl>
F;1529/Modified site: allysine (Lys) #status predicted
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A; Residues: 742-812 <VEN>
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Search completed: May 23, 2001, 16:16:43 Job time: 84 sec

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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PSPD_BOVIN
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CA13_BOVIN
                               CA13_HUMAN
CA34_BOVIN
CA14_CAEEL
YRF2_CAEEL
YRF2_CAEEL
CA1H_HUMAN
CA24_CAEEL
CC34_CAEEL
CC34_CAEEL
CC31_MOUSE
MSRE_MOUSE
C10C_HUMAN
YXWK_CAEEL
CONG_BOVIN
CA11_MOUSE
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CA14_MOUSE
CA54_HUMAN
CA54_CANFA
CA24_MOUSE
CA24_HUMAN
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Q05722
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P17140
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[4] SEQUENCE (MEDLINE-88 Glanville "Amino aci region (78 membrane (Eur. J. Bi [5] SEQUENCE (MEDLINE-88 Babbel W., "Structure amino-acit alpha 1 (1) alpha 1.5.	[3] SEQUEN TISSUE MEDLIN Brazel Deutzm "Compl baseme interr	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-8934043; P SOININEN R., HUCLAR "Structural organiz. type IV collagen."; J. Biol. Chem. 264: [2] SEQUENCE OF 46-1257 TISSUE-Placenta; MEDLINE-88083584; P SOININEN R., HAKA-R "Complete primary s membrane (type IV) FEBS Lett. 225:188-	RESULT 1 CA14_HUMAN ID CA14_HUMAN AC P02465; DT 01-FEB-1996 (Rel.) DT 01-FEB-1996 (Rel.) DT 01-COT-2000 (Rel.) DE COLLAGEN ALPHA 1 (GN COL4AL) OS Homo sapiens (Hum OC Eukaryota; Metazo OC Mammalia; Eutheri OX NCBL_TaxID-9606;	0000004444440000040400040004444444000000
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ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
WITH 2 OTHER CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.
-!- PTM: LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT ARE HYDBOXYLATED IN ALL CASES AND BIND CARBOHYDRATE.
-!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
-!- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
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"The structural genes for alpha 1 and
collagen are divergently encoded on or
overlapping promoter region.";
J. Biol. Chem. 263:17217-17220(1988).
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"The arrangement of intra- and intermolecular disulfide bonds in
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Cheung M.-C., Prockop D.J., Boyd C.D.;
"cDNA clones coding for the pro-alphal(IV) chain of human type
"CDNA clones coding for the pro-alphal(IV) chain of human type
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Them. 260:7681-7687(1985).
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MEDLINE-88112221; PubMed-3338568;
Wood L. Theriault N., Vogeli G.;
"CDNA clones completing the nucleotide and sequence of the alpha 1 chain of basement m
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15-JUL-1999 (Rel. 38, Last annotation update)
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
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collagen IV. Differential evolution of col
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Mammalia; Eutheria;
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J. Biol. Chem.
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Sullivan M., Yamada Y
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PubMed=3597383;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Alpha 1(IV) and alpha 2(IV) collagen genes are regulated bidirectional promoter and a shared enhancer.";
Proc. Natl. Acad. Sci. U.S.A. 85:9679-9682(1988).
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EMBL; J03758; AAA37439.1; -.
EMBL; M23333; AAA51625.1; -.
EMBL; M24694; AAA50292.1; -.
EMBL; X06777; CAA29946.1; -.
EMBL; X02701; CAA26132.1; -.
EMBL; M15832; AAA37340.1; -.
EMBL; M14042; AAA37343.1; -.
EMBL; M13024; -; NOT_ANNOTATED_CDS.
EMBL; M13025; -; NOT_ANNOTATED_CDS.
EMBL; M13026; AAA37344.1; -.
EMBL; M13027; AAA37346.1; -.
EMBL; M13027; AAA37346.1; -.
EMBL; M13027; AAA37346.1; -.
EMBL; M13027; AAA37346.1; -.
EMBL; M13028; AAA37346.1; -.
EMBL; M13028; AAA37346.1; -. PROPEP CHAIN DOMAIN Repeat; Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen;
Extracellular matrix; Col MGD; MGI:88454; Col4a1. InterPro; IPR000087; -. InterPro; IPR001442; -. A33525; CGMS4B ; Hydroxylation; (
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-DEC-1992 (Rel. 24, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.
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                                                   MEDLINE-91169491; PubMed=2004755;
Zhou J., Hostikka S.L., Chow L.T., Tryggvason K.;
"Characterization of the 3' half of the human type
5 gene that is affected in the Alport syndrome.";
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the human type IV collagen
269:6608-6614(1994).
         Eddy R.L., Byers M.G.,
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VARIANTS AS E-400;V-406;V-638;A-638;R-653;R-796;R-869;R-872 & C-1241. MEDLINE-95322976; PubMed-759631; Boye E., Flinter F., Zhou J., Tryggvason K., Bobrow M., Harris A.; "Detection of 12 novel mutations in the collagenous domain of the
                                                                                                              Tryggvason
                                                                                                                          MEDLINE=94010948; PubMed=8406498; Lemmink H.L., Schroeder C.H., Bru
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                                                            van Oost B.A., Smeets H.J.M.;
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vIdentification of four novel mutations
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Rizzoni G., de Marchi M.;
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"Substitution of arginine for glycine 325 in the collagen alpha 5 (IV) chain associated with X-linked Alport syndrome: characterization the mutation by direct sequencing of PCR-amplified lymphoblast
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"Differential splicing of COL4A5
cells: a complex mutation in the
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"Molecular cloning of alpha 5(IV) col
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Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
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"The clinical
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Trivelli A., Pinciaroli A.R., Ragaiolo M., Rizzoni G.F., de Marchi M.;
"Missense mutations in the COL4A5 gene in patients with X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barker D.F., Denison J.C., Atkin C.L., Grego: "Common ancestry of three Ashkenazi-American syndrome and COL4A5 R16770.";
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Tverskaya S., Bobrynina V.,
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Turco A., Heiskari N., Zhou J., Gusmano R., w
Scolari F., Sessa A., Rizzoni G., Tryggvason
Savi M., Ballabio A., de Marchi M.;
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"Detection of mutations in COL4A5 in patients
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Pignatti G.F., Galli L., Bruttin
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MEDLINE-97295089; P
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                                                                                                                                                                   TRIPLE-HELIX DOMAIN ARE INTRODUCED.

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 75 DOMAIN.
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                                                                      UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAIN: PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDII
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ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
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5:197-204(1995).
  DEFECTS
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58:1192-1204(1996).
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  COL4A5
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'- matients with Alport syndrome.
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smano R., Massella L., Banfi G.,
  ASSOCIATED
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Best Local :
                             This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as impositive and this statement is not removed. Use entitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human X-linked hereditary nephritis resulting from a mutation in the gene encoding the alpha 5 chain of co IV.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SAMOYED; TISSUE-Kidney; MEDLINE-94224868; PubMed-8171024; MEDLINE-94224868; PubMed-8171024; Zheng K. Thorner P.S., Marrano P., Baumal R., McInnes R.R.; Zheng K. Thorner P.S., Marrano P., Baumal R., McInnes R.R.; Canine X chromosome-linked hereditary nephritis: a genetic
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Mammalia; Eutheria;
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                                                                                                                                                               IV COLLAGENS.

DISEASE: A DEFECT IN COL4A5 HAS BEEN FOUND TO BE THE CAUSE OF CANINE X-LINKED HEREDITARY NEPHRITIS (HN), A DISEASE SIMILAR THAT IN HUMANS (ALSO REFERED TO AS ALPORT SYNDROME) CHARACTER: BY PROGRESSIVE RENAL FAILURE AND NEUROSENSORY DEAFNESS.

SIMILARITY: TO OTHER TYPE IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                           ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH 2 OTHER CHAINS TO GENERATE TYPE IT COLLAGEN NETWORK.

SUBCELLUAR LOCATION: CELL SURFACE (POIV COLLAGEN NETWORK.

SUBACIA ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-X·Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL.

TRIPLE-HELICAL 7S DOMAIN.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLE REPEATING

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPLEPTIDE REPEATING
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                                                                                                                                                                                                                                                                       UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12
THESE, LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)
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8 (Rel. 36, Last a
LPHA 5(IV) CHAIN (
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Carnivora; Fissipedia;
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Pred. No. 0.014;
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30-MAY-2000 (Rel. 39, Last annotation update)
COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
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                                       MEDIINE-87054581; PubMed-3780963; Schwarz-Magdolen U., Oberbaeumer I., Kuehn K.; Schwarz-Magdolen Sequence of the NC1 domain of the collagen IV and its comparison with alpha 1(IV).";
                                                                                                                                                     terminal 511-residue-long triple-helical segment of the alpha 2(Ichain and its comparison with the alpha 1(IV) chain."; Eur. J. Biochem. 157:49-56(1986).
                                                                                                                                                                                                                               Schwarz U., Schuppan D., Oberbaeumer I., Glanvill Deutzmann R., Timpl R., Kuehn K.; "Structure of mouse type IV collagen. Amino-acid
                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89066738; PubMed-3198626;
Kaytes P. Wood L. Theriault N., Kur
"Head-to-head arrangement of murine t
J. Biol. Chem. 263:19274-19277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete primary structure of mouse alpha Alignment with mouse alpha 1(IV) collagen."; J. Biol. Chem. 264:6318-6324(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89197933; PubMed-2703491;
Saus J., Quinones S., Mackrell A.,
Pihlajaniemi T., Kurkinen M.;
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01-AUG-1988 (Re
                                                                                                                                                                                                                                                                                            SEQUENCE OF 970-1480 FROM N.A. MEDLINE=86220192; PubMed=3011432;
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Mammalia; Eutheria;
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                                                                                                   SEQUENCE OF 1480-1707 FROM N.A. MEDLINE=87054581; PubMed=3780963;
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ne type IV collagen ger
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EMBL; M23334; AAA51626.1; JCEMBL; M23333 AAA51626.1; JCEMBL; J04695; AAA50293.1; EMBL; J04448; AAA57438.1; EMBL; X04647; CAA28308.1; EMBL; X04410; CAA27998.1; EMBL; X02896; CAA26655.1; EMBL; X02897; CAB51614.1; EMBL; X02898; CAA26657.1; EMBL; X02898; CAA26657.1; EMBL; X02899; CAA26658.1; EMBL; X02899; CAA26657.1; EMBL; X02899; CAA26658.1; EMBL; X02899; CAA26659; EMBL; X02899; CAA26659; EMBL; X02899; CAA26659; EMBL; X02899; CAA2665
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ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

NITH 2 OTHER CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NCI) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.

TRIPLE-HELICAL 7S DOMAIN.

NIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

ONIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF THESE, LOCATED IN THE NCI DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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"Extensive homology between the carboxyl-terminal peptides of mouse alpha 1(IV) and alpha 2(IV) collagen.";
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Vogeli G., Horn E
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"Proposed alignment of helical interruptions"
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"Human basement membrane collagen (type IV). The amino acid sequence
of the alpha 2(IV) chain and its comparison with the alpha 1(IV)
chain reveals deletions in the alpha 1(IV) chain.";
Eur. J. Blochem. 172:35-42(1988).
                                                                                                                                                                                                                                                                                        MEDLINE-89066769; PubMed-3198637;
Hostikka S.L., Tryggvason K.;
"The complete primary structure of the alpha
collagen and comparison with the alpha 1(IV)
J. Biol. Chem. 263:19488-19493(1988).
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            Hostikka S.L., Kurkinen M., Tryggvason K.;
"Nucleotide sequence coding for the human type IV collagen alpha chain cDNA reveals extensive homology with the NC-1 domain of ali (IV) but not with the collagenous domain or 3'-untranslated region.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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01-FBB-1991 (Rel. 17, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
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of basement-membrane type IV collagen.";
Eur. J. Biochem. 176:617-624 (1988).
-I- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE', MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Siebold B., Deutzmann R., Kuehn K.; "The arrangement of intra- and intermolecular carboxyterminal, non-collagenous aggregation e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region of human collagen type IV divergent transcription."; Blochem. J. 292:687-695(1993).
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Fischer G., Schmidt C., Opitz J., Cully Z., Kuehn K., Poeschl E.;
"Identification of a novel sequence element in the common promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen are divergently encoded on coverlapping promoter region.";
J. Biol. Chem. 263:17217-17220(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           separated by a bidirectional EMBO J. 7:2687-2695(1988).
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Myers J.C., Howard P.S., Jelen A.M., Dion A.S.,
"Duplication of type IV collagen COOH-terminal
specific expression of alpha 1(IV) and alpha 2
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                                                                                                                                                                   SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN UNETWORK:
DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CERMINIS, FREQUENT INTERRUPTIONS (WHICH HELE CLASSE FLEXIBILITY IN THE TRIPLE HELICAL DOMAIN (WHICH HELE CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE HELICAL 7S DOMAIN.
                                                         PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPHUNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS PTM: TYPE IV COLLAGENS CONTAIN UNDERGUS CYSTEINE RESIDUES ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                   NIDOGEN.
IV COLLAGENS.
                              VOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
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use modified the This SWISS-PROT entry is copyright. It is produced through a between Agen the Sylss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content non-profit institutions as long and this statement is not remove is not removed (See http://www.isb-sib Usage by he EMBL outstation restrictions on interest is in no we and for collaboration . L outstation . .ch/announce/ in no way

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Best Local Similarity
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EMBL; M36963; AAA53099.1; -
EMBL; X12784; CAA31275.1; -
EMBL; J04217; AAA53097.1; -
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Christiano A.M., Rosenbaum L.M.,
Christiano T.T., Pan T.C., Zhang R.
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Q02388; Q14054; Q16507;
Q1-JUN-1994 (Rel. 29, Created)
Q1-FEB-1996 (Rel. 33, Last sequence up
Q1-OCT-2000 (Rel. 40, Last annotation
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR
                                                                                                                                                                                                                            1368
                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                   Christiano A.M., Greenspan D.S., Lee S., Uitto J.; "Cloning of human type VII collagen. Complete primary sequence of alpha 1(VII) chain and identification of intragenic polymorphisms. J. Biol. Chem. 269:20256-20262(1994).
                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      SEQUENCE
                                                                                 MEDLINE=94327588;
                                                                                        SEQUENCE FROM N.A.
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PF01391; Collagen;
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Basement membrane; Collagen; Signal
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M -> I (IN REF. 5).
G -> H (IN REF. 9).
H -> G (IN REF. 9).
H -> G (IN REF. 9).
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VARIANT DDEB SER-2040.

WARIANT DDEB SER-2040.

MEDLING-94224777; PubMed-8170945;

Christiano A.M., Ryynaenen M., Uitto J.;

"Dominant dystrophic epidermolysis bullosa: i
"Dominant dystrophic in the triple-helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARIANT RDEB LYS-2798.

MEDLINE-93291877; PubMed-8513326;

Christiano A.M., Greenspan D.S., Hoffman G.G., Zh
Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;

"A missense mutation in type VII collagen in two
with recessive dystrophic epidermolysis bullosa."

"A missense mutation in type VII collagen in two
with recessive dystrophic epidermolysis bullosa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=94375010; PubMed=8088784;
Christiano A.M., Hoffman G.G., Chung-Honet L.C.,
                                 MEDLINE-96081220;
Christiano A.M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jaervikallio A., Pulkkinen L., Uitto J.; "Molecular basis of dystrophic epidermolysis the type VII collagen gene (COL7A1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uitto J., Greenspan D.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion proteins involved in tissue-specific organization of extracellular matrix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino-terminal and chimeric. Homology to cartilage matrix protein, the type III domains of fibronectin and the A domains of von Willebrand factor.";
                                                                                                            VARIANT PEB-DDEB CYS-2623
                                                                                                                                                                                                                 collagen
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Bauer E.A., Mattei M.-G., Chu M.-L., Uitto
"Human type VII collagen: cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 815-1439 FROM N.A. MEDLINE=91334380; PubMed=1871109;
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dystrophic epidermolysis bullosa provides molecular mechanisms underlying defective
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Hovnanian A., Rochat A., Bodemer C., Petit E.,
Fraitag S., Christiano A.M., Uitto J., Lathrop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uitto J., Pope F.M., Eady R.A.J.;
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J. Invest. Dermatol. 107:171-177(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Christiano A.M., McGrath J.A., Uitto J.;
"Influence of the second COL7A1 mutation in phenotypic severity of recessive dystrophic J. Invest. Dermatol. 106:766-770(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genotype/phenotype correlation in a case severity."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular mechanisms formation.";
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Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T.,
"Molecular basis of recessive dystrophic epidermolysis b
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MEDLINE-96154068;
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MEDLINE-96220218; PubMed-8644729;
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MEDLINE-95164985; Pubn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of 18 new mutations in COL7A1 in
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helical domain
              PIM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HUDROXYLATED IN SOME OR ALL OF THE CHAINS. DISEASE: DEFECT IN COLTAI IS A CAUSE OF RECESSIVE DYSTROPHIC EPIDERMOLYSIS BULLOSA (EB); A GROUP OF BLISTERING SKIN DISEASE CHARACTERIZED BY TISSUE SEPARATION WITHIN THE DEBNAL-EPIDERMAL BASEMENT MEMBRANE ZONE. THE DYSTROPHIC TYPE, THE SCARRING FORM MANIFESTS THE CLEAVAGE WITHIN THE PAPILLARY DERMIS BLOW THE BASAL LAMINA AT THE LEVEL OF THE ANCHORING FIBRILS. BOTH AUTOSOMAL DOMINANT AND RECESSIVE INHERITANCE PARTHRIS HAVE BEEN RECOGNIZED. DISEASE: EPIDERMOLYSIS BULLOSA ACQUISITA (EBA) IS AN AUTOIMMUNE ACQUIRED BLITTERING SKIN DISEASE RESULTING FROM AUTOANTIBODIES TO
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                                                                                                                                                                                                                                                                                                                       FUNCTION: STRATIFIED SQUAMOUS ÉPITHELIAL BASEMENT MEMBRANE PROTEIN THAT FORM ANCHORING EIBRILS WHICH MAY CONTRIBUTE TO EPITHELIAL BASEMENT MEMBRANE ORGANIZATION AND ADHERENCE BY INTERÁCTING WITH EXTRACELLULAR MATRIX (ECM) PROTEINS SUCH AS TYPE IV COLLAGEN. SUBUNIT: HOMOTRIMER.
TYPE VII COLLAGEN
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f type VII collagen.";
4:1579-1583(1995).
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DISEASE:

DEFECT

IN COL7A1 IS A CAUSE OF DEB IS A BLISTERING SKIN

DYSTROPHIC DISEASES W

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EPIDERMOLYSIS

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Best Local (
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Q01955;
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               Goodpasture antigen (alpha 3(IV)NC1). Identifica antigenic region at the triple hellx/NC1 domain J. Biol. Chem. 267:19780-19784(1992).
                                                            MEDLINE=93015826; PubMed=1400291;
Quinones S., Bernal D., Garcia-Sogo M., Elena S.F.,
"Exon/intron structure of the human alpha 3(IV) gend
                                                                                                                                                                                                                                         Mariyama M., Leinonen A., Mochizuki T., Tryggvason K., Reeders S.T., "Complete primary structure of the human alpha 3(IV) collagen chain. Coexpression of the alpha 3(IV) and alpha 4(IV) collagen chains in
                                                                                                                                                                                                                                                                                                                                                                    COL4A3.
COL4A3.
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata;
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01-OCT-2000
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                                                                                                               SEQUENCE OF 1386-1670
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SIMILARITY: CONTAINS 1 PROTESS INHIBITOR DOMAIN BPTI/KUNITZ FAMILY OF INHIBITORS.

SIMILARITY: CONTAINS 9 FIBRONECTIN TYPE III-LIKE CAUTION: REF. 5 SEQUENCE DIFFERS FROM THAT SHOWN I
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SIMILARITY: THE NC-1 DOMAIN OF TYPE VII COLLAGEN HAS HOMOLOGY
SIMILARITY: TYPE III DOMAINS, VON WILLEBRAND FACTOR A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHERITANCE. ULTRASTRUCTÚRALLY, DEB IS CHARACTERIZED BY TISSUE SEPARATION WHICH OCCURS BELOW THE DERMAL-EPIDERNAL BASEMENT MEMBRANE AT THE LEVEL OF THE ACCHORING FIBRILS. THE MOST SEVERE FORM OF RDEB IS THE HALLOPEAU-SIEMENS TYPE (HS-RDEB), A MILDER FORM IS THE MITIS TYPE (M-RDEB), AND THERE ARE STILL THE INVERSE, AND THE LOCALIZED TYPES. CLINICALLY, HS-RDEB MANIFESTS WITH MUTILATING SCARRING, WITH JOINT CONTRACTURES, CORNEAL EROSIONS, ESOPHAGUS STRUCTURES, AND PROPENSITY TO FORMATION OF CUTANEOUS SOUGHOUS CELL CARCINOMAS LEADING TO PREMATURE DEMISE OF THE AFFECTED INDIVIDUALS. M-RDEB SHOWS LIFELONG BLISTERING TENDENCY, MITH LIMITED SCARRING AND LESS FREQUENT EXTRACUTANEOUS MITH LIMITED SCARRING AND LESS FREQUENT EXTRACUTANEOUS
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INHERITANCE. ULTRASTRUCTURALLY, DEB IS CHARACTERIZED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration {f \cdot} en the Swiss Institute of Bioinformatics and the EMBL outstation {f \cdot}
                                                                                                                                                                                                                               tissues.
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                         rpile 3(1V) gene encompassing the
Identification of a potentially
NC1 domain junction.";
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SEQUENCE OF 1453-1670 FROM N.A.

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Lemmink H.H., MoChizuki T., van den Heuvel L.P.W.J., Schroeder C. Barrientos A., Monnens L.A.H., van Oost B.A., Brunner H.G., Reeders S.T., Smeets H.J.M.;

"Mutations in the type IV collagen alpha 3 (COL4A3) gene in autos recessive Alport syndrome.";

Hum. Mol. Genet. 3:1269-1273 (1994).

Hum. Mol. Genet. 3:1269-1273 (1994).

-!- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE' MESSHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The human mRNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-29 FROM N.A.
MEDLINE-98196854; PubMed-9537506;
Momota R., Sugimoto M., Ochashi T., Kigasawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng L., Xia Y., Wilson C.B.;
"Alternative splicing of the NC1 domain of the human alpha 3(IV)
collagen gene. Differential expression of mRNA transcripts that
predict three protein variants with distinct carboxyl regions.";
C. Biol. Chem. 269:2342-2348(1994).
                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT PRO-1474.
MEDLINE=95078827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spliced."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1993) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1644-1670 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Turner N., Mason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrison K.E., Mariyama M., Yang-Feng T.L., Reeders S. "Sequence and localization of a partial cDNA encoding 3 chain of type IV collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93280184; PubMed=8505332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 424:11-16(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94124597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to be the alpha :
J. Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1331-1670 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ninomiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of the human Goodpasture antigen demonstrates to be the alpha 3 chain of type IV collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pusey C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92147878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91353570; PubMed=1882840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE OF 1439-1670,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol.
COCHLEA, LUNG AND BRAIN.

DOMAIN: ALPHA CHAINS OF TYPE IV CO
DOMAIN (NC1) AT THEIR C-TERMINUS,
G-X-Y REPEATS IN THE LONG CENTRAL
CAUSE FLEXIBILITY IN THE TRIPLE HE
TRIPLE-HELICAL 7S DOMAIN.
                                                                                                                                       C-TERMINAL NC1 DOMAINS.
TISSUE SPECIFICITY: ALPHA 3 AND COLOCALIZED AND PRESENT ONLY IN
                                                                                                                                                                                                                                                                                               NIDOGEN.
SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hain of type IV collagen.";
J. Hum. Genet. 49:545-554(1991).
                                                                                                                                                                                                          SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL)
ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (
3/L5; ARE PRODUCED BY ALTERNATIVE SPLICING. TH
                                                                                                                                                                                                                                                                                    WITH
                                                                                                                                                                                                                                                                               ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCT WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
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89:592-601(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1737849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=7987301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S., Saus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Goodpasture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R., Fox M., Povey S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding for the human alpha3(IV) and arranged head-to-head on chromosom
                                                                                                                                            BASEMENT
                            HELIX),
                                                                                               COLLAGEN
                                               OLLAGEN HAVE A NONCOLLAGENOUS FREQUENT INTERRUPTIONS OF THE TRIPLE-HELICAL DOMAIN (WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLICING
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                            AND
                                                                                                                                          TYPE IV COI
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                            A SHORT
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EMBL; M92993; AAA21610.1;

EMBL; S55790; AAB19637.1;

EMBL; M81379; AAA51556.1;

EMBL; L08650; AAA52044.1;

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EMBL; U02520; AAA18943.1;
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InterPro; IPR001442; ...
Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 21.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Basement membrane; Collagen; Signal; Cell adhesion Alternative splicing; Polymorphism; Phosphorylation.
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DOMAIN
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PTM: THE ALTERNATIVE SPLICED FORM V CONTAINS AN ADDITIONAL
N-LINKED GLYCOSYLATION SITE.
PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE IDISEASE: DEFECTS IN COL4A3 ARE ASSOCIATED WITH THE TYPE I AUTOSOMAL RECESSIVE FORM OF ALPORT SYNDROME, AN HEREDITARY GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE FENAL FAHEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY IMALES AND FEMALES.
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120070; -.
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                                                                 CELL ATTACHMENT SITE (POTENTIAL).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                               EMBL; M69077; AAA32460.1; -. EMBL; M55568; AAA32446.1; -. PIR; B46345; B46345.
                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the 
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                                                                                                                                 entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE MEDLINE-90320115; PubMed-2196741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage PRD1.
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               CNIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90206069;
                                                                                                                                                                                                                                               FUNCTION: THE SHORT COLLAGEN-LIKE REGION IS PROPOSED TO ACT AS TRIMERIZATION SIGNAL LEADING TO THE FULFILLMENT OF THE SYMMETRY REQUIREMENT OF THE MINOR CAPSOMER.

SUBUNIT: THE PRDI VIRION IS COMPOSED OF AN ICOSAHEDRAL PROTEIN COAT, AN INNER PROTEIN-LIPID MEMBRANE, AND A DSDNA GENOME WHICH IS LOCATED INSIDE THE LIPID VESICLE. THE PROTEIN COAT CONSISTS MAINLY OF PROTEIN P3. THE MINOR PROTEIN P5 IS ALSO CONSIDERED TO CONSTITUTE PART OF THE PROTEIN COAT.

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
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D PROTEIN (PROTEIN P5).
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            EMBL; M92642; AAA58427.1; -. EMBL; S57132; AAB25797.1; -. PIR; S23810; S23810.
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RESULT 10
CA1F_HUMAN
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COLIGAI.
Homo sapiens (Human).
Homo sapiens (Human).
Metazoa; Chordata;
Metazoa; Primates;
use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              WITH OTHER TYPES OF COLLAGEN.

- I- DEVELOPMENTAL STAGE: TRANSIENTLY ELEVATED EXPRESS GESTATION, AND DECREASE AT TERM.

- I- DOMAIN: THIS SEQUENCE DEFINES EIGHTEEN DIFFERENT TRIPLE-HELICAL DOMAINS (COL9 TO COL1) AND TEN NON DOMAINS (COL9 TO COL1)
                                                                                                                                                                                                                                                                                                                                                                                                               THE NUMEROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE THIS MOLECULE EITHER ELASTIC OR FLEXIBLE.

-!- TISSUE SPECIFICITY: IN THE PLACENTA, WHERE IT IS FOUND IN THE AMNION, A MEMBRANOUS TISSUE LINING THE AMNIOTIC CAVITY. WITHIN THE AMNION, IT IS FOUND IN AN ACELLULAR, RELATIVELY DENSE LAYER OF A COMPLEX NETWORK OF RETICULAR FIBERS. ALSO LOCATED TO A FIBROBLAST LAYER BENEATH THIS DENSE LAYER. EXISTS IN TISSUES IN ASSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92335339; PubMed-1631157; Pan T.C., Zhang R.Z., Mattel M.-G., Timpl R., Chu M.-L.; Pan T.C., Zhang R.Z., Mattel M.-G., Timpl R., Chu M.-L.; "Cloning and chromosomal location of human alpha 1(XVI) collagen."; Proc. Natl. Acad. Sci. U.S.A. 89:6565-6569(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA1F_HUMAN Q07092;
                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cysteine-containing non-collagenous J. Biochem. 112:856-863(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and partial characterization of a novel collagen
chain, alpha 1(XVI), consisting of repetitive collagenous domains a
                                                                                           the European Bioinformatics Institute.
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Kanamori T., Yamakoshi H., Nagai Y.;
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PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING PTM: PROLINES AT THE THIRD POSITION OF ALL OF THE CHAINS.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

SIMILARITY: BELONGS TO THE FAMILY OF FIBRIL-ASSOCIATED COLLAGEN: WITH INTERRUPTED HELICES (FACIT).
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                          chain.
                                                   TISSUE=Kidney;
MEDLINE=95014445;
                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-OCT-1996 (Rel. 34,
01-OCT-2000 (Rel. 40,
COLLAGEN ALPHA 4(IV)
                                                                                                                                                                                CA44_HUMAN
                                MEDLINE-95014445; PubMed-7523402;
Leinonen A., Mariyama M., Mochizuki T., Tryggvason K., Reeders S.T.
"Complete primary structure of the human type IV collagen alpha 4(1
                                                                       SEQUENCE
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Pfam; PF01391; Collagen; 16.
[2]
                                                                                        NCBI_TaxID=9606;
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        Biol.
               n. Comparison chains.";
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                                                                      FROM N.A.
                                                                                        s (Human).
Metazoa; Chordata; C
Metazoa; Primates; C
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738
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        269:26172-26177(1994)
                                                                                                                                                                                 STANDARD;
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                        structure with struc
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                                                                                                                                     CHAIN
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Last annotation update)
CHAIN PRECURSOR.
                                                                                                                                                               Created)
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                          structure
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TRIPLE-HELICAL REGION 1 (
WITH 2 MPERFECTIONS
NONHELICAL REGION 1 (NC1)
RDA -> GGR (IN REP. 2).
R -> P (IN REF. 2).
T -> P (IN REF. 2).
T -> P (IN REF. 2).
T -> P (IN REF. 2).
S -> P (IN REF. 2).
T -> P (IN REF. 2).
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Pred. No.
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TRIPLE-HELICAL REGION 3 (CO)
NONHELICAL REGION 3 (NC3)
                                                                                                                                                                                                                                                                                                                                                                                                                                             TRIPLE-HELICAL REGION 4 (COL4) WITH 2 IMPERFECTIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONHELICAL REGION 9 (N
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                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NONHELICAL REGION 5
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NONHELICAL REGION 7 (NC7)
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COLLAGEN ALPHA
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                        he human type IV and expression
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ION 10 (NC10).
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Lemmink H.H., Nillesen W.N., Mochizuki T., Brunner H.G., van Oost B.A., Monnens L.A.H. "Benign familial hematuria due to mutation alpha4 gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99011253; PubMed=9792860;
BOYE E., Mollet G., Forestier L., Cohen-Solal L., Heidet L.,
Cochat P., Gruenfeld J.-P., Palcoux J.-B., Gubler M.-C., Antignac
"Determination of the genomic structure of the COL4A4 gene and of
novel mutations causing autosomal recessive Alport syndrome.";
Am. J. Hum. Genet. 63:1329-1340(1998).
Am. J. Hum. Genet. 63:1329-1340(1998).
-i- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT OF
GLOMEROLAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
MESHWORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOChizuki T., Jenuary Mochizuki T., Jenuary Mochizuki T., Verellen-Dumoulin C., Chan B., Schiuever C..... Smeets H.J., Reeders S.T.;

"Identification of mutations in the alpha 3(IV) and alpha "Identification of mutations in the alpha 3(IV) and alpha "Identification of mutations in an alpha 10 per syndrome.";
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Lemmink H.H., Schroeder C.H., Monnens L.A.H., Smeets H.J.M.;
"The clinical spectrum of type IV collagen mutations.";
Hum. Mutat. 9:477-499(1997).
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                                                                                                                COCHLEA, LUNG AND BRAIN.

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN: ALPHA CHAINS OF THE FORTH OF THE LORD OF THE G-X-Y REPEATS IN THE LORG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH I CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER-AND INTRAMOLECULAR DISULFIDE BONDING. 12
                                                                                                                                                                                                                                                                                       NIDOGEN.
SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1 (
ALPHA 6 (IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTU
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV COLLAGENS
COLOCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANES OF KIDN
                                                                                  THESE, LOCATE
IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes in autosomal recessive et. 8:77-82(1994).
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shi T., Yoshioka
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partial gene
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H., Smeets H.J.
n of the type T
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X STRUCTURE
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GLOMERULONEPHROPATHY CH. HEMATURIA AND DEAFNESS. DISEASE: DEFECTS IN AUTOSOMAL RECESSIVE

COLAAA ARE ASSOCIATED WITH THE TYPE II
FORM OF ALPORT SYNDROME (AS), AN HEREDITARY
(CHARACTERIZED BY PROGRESSIVE RENAL FAILURE,
ESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEE

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EMBL; D17391;
MIM; 120131; -
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CARBOHYD
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Pfam; PF01391; Collagen; 20.
Extracellular matrix; Connective tissue; Basement membrane; Repeat;
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SIMILARITY: TO OTHER TYPE IV COLLAGENS.
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1686 (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                 E (IN FBH)
                                                                                                                                                                                                       (IN AS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGION (NC1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
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Best Local
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_ASCSU
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA24_ASCSU STANDARD; PRT; 1763 AA. P27393; P17409-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
                                                       CHAIN
                                                                                    Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen;
Hydroxylation; Connective
Alternative splicing; Gly
                                                                                                                                          EMBL; M67507; AAA18014.1;
PIR; S16366; S16366.
InterPro; IPR000087; -.
InterPro; IPR001442; -.
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-91340768; PubMed-1714907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
                              DOMAIN
                                          DOMAIN
                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ascarididae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pettitt J., Kingston I.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVKGDKGNPGWPGAP
|::||:||:|| || |
184 GIQGDRGDPGLPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND II; ARE PRODUCED BY ALTERNATIVE SPLICING.

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G.Y.Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (HHICH M CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.

TRIPLE-HELICAL 7S DOMAIN.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                       IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
9; Conserv
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1690 AA;
 1530
1548
                                                                                   splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ascaris.
                                                                                   Connective tissue; B licing; Glycoprotein;
26
1763
42
1529
1763
1637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
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POTENTIAL.

COLLAGEN ALPHA 2(IV) CHAIN.
7S DOMAIN.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
OR 1634 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61; DB 1;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> FE (IN REF. 2).
E1E72F283A72BAAE CRC64;
                                                                                                  Basement membrane;
                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1690
                                                                                                   Repeat; Collagen;
                                                                                                                                                                                                                                                                                                                                                  E BONDING. 12 OF
ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAY
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                                                                                                                                                                                        RT "Structural similarity between bovine conglutinin and bovine lung rt surfactant protein D and demonstration of liver as a site of rt synthesis of conglutinin.";

RT Synthesis of conglutinin.";

RL Immunology 78:159-165(1993).

CC -1- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER CENTRACELLULAR REPRACHEDSYL MOIETIES. IT COULD PARTICIPATE IN THE EXTRACELLULAR COMPLEX OF 4 SET OF PULMONARY SURFACTANT.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- SUBCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL COLLAGENOUS AND SP-D) AND 2 SMALL CLINEDROPHOBEL PROTEINS (SP-B AND SP-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P35246;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
PULMONARY SURFACTANT-ASSOCIATED PROTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
InterPro; IPR000087; -- InterPro; IPR001304; -- Pfam; PF01391; Collagen
                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93170856;
Lim B.L., Lu J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSPD_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                        HSSP; P19999;
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                                                  x75911; CAA53510.1; S33603; S33603.
                                                                                                                                                       SWISS-PROT entry is copyright: It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLPGMKGNPGLPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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1593
1656
1690
1702
126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                         Reid K.B.M
                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8436402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos.
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1599
1752
1749
1709
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73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR 1637 (BY SIMILARITY).
BY SIMILARITY.
OR 1749 (BY SIMILARITY).
OR 1752 (BY SIMILARITY).
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (IN FORM II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDIGPAGPPGPPGPREFTGSGSIVGPRGHSGDKGVK (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEQGPRGPQGPPGPVPSTGAKGTIIGPEGAPGMKGEK ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; actyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ration update)
proTEIN D PRECURSOR (SP-D) (PSP-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1637 (BY SIMILARITY). SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                     http://www.isb-sib.ch/announce/
                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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                                                                                                                 bу
                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovoidea;
                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                  collaboration
                                                                                                                                                       outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                    commercia
                                                                                                                               no
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RESULT 14
CA44_RABIT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                           Kamagata Y., Mattei M.-G., Ninomiya Y.;

"Isolation and sequencing of cDNAs and genomic DNAs encoding the alpha 4 chain of basement membrane collagen type IV and assignmen the gene to the distal long arm of human chromosome 2.";

J. Biol. Chem. 267:23753-23758(1992).

-i- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update
COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                           TISSUE=Corneal endothelium; MEDLINE=93054733; PubMed=1429714;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COL4A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA44_RABIT P55787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00059; lectin_c; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
                                            <del>-</del>
                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Lectin; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GLKGERGAPGEPGAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                            SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1(IV)-
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).
DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH M
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GVKGDKGNPGWPGAP
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHERE ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN IV COLLAGENS.
                                                                       PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                MESHWORK TOGETHER WITH LAMININS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345
90
78
87
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96
165
171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collagen;
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
248
369
359
359
78
78
96
165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.

COLLAGEN-LIKE.
COLLAGEN-LIKE.
COLLED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL
HYDROXYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PULMONARY
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RESULT 1
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Best Local Similarity
Matches 10; Conser
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DOMAIN
DOMAIN
          mRNAS by estradiol in the immature rat uterus.";
DNA 7:347-354(1988).
-I- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONN
ALONG WITH TYPE I COLLAGEN.
-I- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. TINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS.
ALSO CROSS-LINKED VIA HYDROXYLYSINES.
                                                                                                                                                                              "Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. "Cloning of cDNA for rat pro alpha 1(III) collagen and expression patterns of type I and type III collagen and genes in experimental granulation tissue.";
Biochim. Biophys. Acta 1217:41-48(1994).
                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ex
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L01477; -; NOT_ANNOTATED_CDS. InterPro; IPR000087; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                          SEQUENCE OF 308-482 FROM N.A. MEDLINE-88296083; PubMed-2456
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94114571; PubMed=8286415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01391; Collagen; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                      Regulation of alpha 2(I),
                                                                                                                              Frankel F.R., Hsu C.-Y.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVKGDKGNPGWPG
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                                                                                                                 B., Mohn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             matrix; Connective tissue; Repeat; Hydroxylation; Basement membrane; Collagen; Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                          PubMed=2456904;
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                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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499
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616
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76.9%;
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NONHELICAL REGION (NC1).
OR 499 (BY SIMILARITY).
OR 502 (BY SIMILARITY).
BY SIMILARITY).
OR 616 (BY SIMILARITY).
OR 619 (BY SIMILARITY).
BY SIMILARITY).
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Pred
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OF THE
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                        THE CHAINS
                                                                                                                                                                                                         fibronectin
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                     MEDLINE-80026027; PubMed-488907;
Dewes H., Fletzek P.P., Kuhn K.;
"The covalent structure of calf skin t
acid sequence of the cyanogen bromide
(positions 223-402).";
                                                                                                                                     acid
                                                                                                                                                                      SEQUENCE OF 1-242.
MEDLINE=80026026; PubMed=488906;
Fietzek P.P., Allmann H., Rauter
                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                                                                                                                                                                  20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
COLLAGEN ALPHA 1(III) CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000087; ...
InterPro; IPR000085; ...
InterPro; IPR001007; ...
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 6.
PROSITE; PS01208; VWFC; PARTIAL.
Extracellular matrix; Connective tissue; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                  CA13_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                              Kuhn
                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                         Bos taurus
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                                                                                     SEQUENCE OF 243-422.
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                                                                                                                      covalent structure of calf skin type III collagen. I. The amino sequence of the amino terminal region of the alpha 1(III) chain itlons 1-222).";
                                                                                                                                                                                                                                                                                                                                                                                                                                GVKGERGSPGGPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A29905; A29905.
S41067; S41067.
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                                                                                                                                                                                                                                                                           (Bovine)
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376
369
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369
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             Physiol. Chem. 360:821-832(1979)
                                                                                                             Physiol.
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636
368
368
369
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Pred. No.
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INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                             360:809-820(1979)
                                                                                                                                                                      J.
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                                  type III collagen.
e peptide alpha 1(II
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                                                                                                                                                                        Henkel W., Wachter E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydroxylation;
                                                                                                                                                                                                                                                   Pecora; Bovoidea;
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                                  gen. II. The amino 1(III)CB1,8,10,2
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RESULT 17
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Best Local
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CARBOHYD
 CA13_HUMAN P02461;
                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
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"The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the carboxyterminal cyanogen bromide peptide alpha 1(III)CB9B (positions 928-1028).";
HOPPE-Seyler's Z. Physiol. Chem. 360:861-868(1979).
-i- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bentz H., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. II amino acid sequence of the cyanogen bromide peptide alpha (positions 403-551).";
                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80026030;
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InterPro; IPR001007; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler's Z. Physiol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=80026028; PubMed=488908;
                                                                           702 GVKGERGSPGGPGA 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALONG WITH TYPE I COLLAGEN.
SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS.
LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALSO CROSS-LINKED VIA HYDROXYLYSINES.
                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: PROLINES AT THE THIRD POSITION OF THE TRUNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL A02862; CGB07S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s H., Fletzek P.P., Kuhn K.;
covalent structure of calf skin type III collagen. V. The amino sequence of the cyanogen bromide peptide alpha 1(III)CB9A ition 789-927).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H., Glanville R.W., Fietzek P.P., Kuhn K.; covalent structure of calf skin type III collagen. IV. The sequence of the cyanogen bromide peptide alpha 1(III)CB5 itlons 552-788).":
                                                                                                   GVKGDKGNPGWPGA
                                                                                                                                        Similarity
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1041
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107
119
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950
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                                                                                                                                                                                                                                                                                                                                                                matrix; Connective tissue; Repeat; Hydroxylation;
             STANDARD;
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71.4%;
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                                                                                                                                                                                                                                                                HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                      Score 60;
Pred. No.
                                                                                                                                                                                        INTERCHAIN.
8; 8EEC33D1C66EC9A3 CRC64;
                                                                                                                                                                                                                            CROSS-LINK SITE
                                                                                                                                                                                                                                                                                                     TRIPLE-HELICAL REGION NONHELICAL REGION HYDROXYLATION.
                                                                                                                                                                                                                 INTERCHAIN
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           PRT;
                                                                                                                            Mismatches
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           1466 AA
                                                                                                                                      DB 1;
0.19;
                                                                                                                           <u>بب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                               (C-TERMINAL)
                                                                                                                                                                                                                                                                                                                                        (N-TERMINAL).
                                                                                                                                                  Length 1049;
                                                                                                                           Indels
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na 1(III)CB4
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                                                                                                                         Gaps
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REVISIONS.
Seyer J.M.
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01-JAN-1990 (Rel. 13,
01-OCT-2000 (Rel. 40,
COLLAGEN ALPHA 1(III)
         procollagen.";
Nucleic Acids Res.
                                "Molecular cloning ar
                                                         MEDLINE=85087944; PubMed=6096827; Loidl H.R., Brinker J.M., May M.,
                                                                                     SEQUENCE OF 1065-1466 FROM N.
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Mammalia; Eutheria;
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MEDLINE=77134724; Pu
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MEDLINE=89350838; PubMed=2764886;
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"A mutation in the gene for Lar.
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associated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels.";
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MEDLINE-81208139; PubMed-7016180
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MEDLINE=89109135; PubMed=2492273;

Tromp G., Kulvaniemi H., Shikata H., Prockop D.J

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MEDLINE-92316511; PubMed-1352273;
Richards A.J., Ward P.N., Narcisi P.,
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    Eukaryota;
              Bos taurus
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MEDLINE-93022543; PubMed-1357232;
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f the triple helical region of type III
nlers-Danlos syndrome type IV.";
28:458-463(1991)
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ALPHA 6(JV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.

-I- SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

-I- DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.

-I- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HUDROXYLATED IN SOME OR ALL OF THE CHAINS.

-I- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISGLETIOE BONDING. 12 OF
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane collagen.".

J. Biol. Chem. 262:7874-7877(1987).

-i- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GBM), FORMING A 'CHICKEN-WIRE MESHMORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                        Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Basement membrane; Collagen; Cell adhesion.
                                                                                                                                                    Pfam; PF01413; C4; 2. Pfam; PF01391; Collagen; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91093146; PubMed=1985905;
MOTITISON K.E., Germino G.G., Reeders S.T.;

"Use of the polymerase chain reaction to clone and sequence a encoding the bovine alpha 3 chain of type IV collagen.";

J. Biol. Chem. 266:34-39(1991).
                                  DOMAIN
                                                                                                                                                                                                                                                                               EMBL; M63139; AAA62708.1; -.
                                                                                                                                                                                                                   InterPro; IPR000087; -. InterPro; IPR001442; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Butkowski R.J., Langeveld J.P.M., Wieslander J., Hamilton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of collagen IV."
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87222419; PubMed=2438283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 227-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of the Goodpasture antige"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saus J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 227-258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Localization of the Goodpasture epitope to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER TYPE IV COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem. 263:13374-13380(1988).
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a 3(IV) chain
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RESULT 19
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Best Local Similarity
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P17139;
O1-AUG-1990 (Rel. 1
O1-MAR-1992 (Rel. 2
O1-NOV-1997 (Rel. 2
                                                                                                                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M. Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Lightning J., Lloyd C., Mortimore B., O'Callaghan Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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01-MAR-1992 (Rel. 21, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
EMB-9 OR CLB-2 OR K04H4.1.
                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                  Guo X., Kramer J.M.;
                                                                                                 MEDLINE=90008929; PubMed=2793871;
                                                                                                             STRAIN-BRISTOL N2;
                                                                                                                        SEQUENCE OF 1446-1758 FROM N.A.
                                                                                                                                                  Nature
                                                                                                                                                                "2.2 Mb of elegans.";
                                                                                                                                                                                      Wohldman P
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       collagen
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"Embryonic lethality caused by mutations in basement membrane
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE-91141582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae; Caenorhabditis
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                                                                     "The two Caenorhabditis elegans basement membrane (type IV) collagen
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                                                                                                                                                368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                        en of C. elegans.";
349:707-709(1991).
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                                                                                                                                                                        contiguous nucleotide sequence from chromosome
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INTERACTIONS
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C03B66F14E7008DE CRC64;
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InterPro; IPR0000887; -.
InterPro; IPR001442; -.
InterPro; IPR001442; -.
Pfam; PP01413; C4; 2.
Pfam; PP01391; Collagen; 22.
Extracellular matrix; Connective tissue; Basement membrane;
Extracellular matrix; Connective tissue; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B34476; B34476.
PIR; S13651; S13651.
WormPep; K04H4.1; CE00246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X56979; CAA40299.1; -. EMBL; Z27078; CAA81584.1; -. EMBL; J05067; AAB59179.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NCI) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IV COLLAGENS
 GVKGEKGLPGPPGPP 238
                         GVKGDKGNPGWPGAP 15
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7 MW; 7083D9AF63E05E
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G -> R (IN REF. 2).

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PG -> TR (IN REF. 2).
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OR 1751 (BY SIMILARITY).

OR 1754 (BY SIMILARITY).

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BY SIMILARITY.

G -> E (IN MUTANT G34).

G -> E (IN MUTANT G23/HC70.

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1; Mismatches
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VLRVSLECPDLLDLQGNLDKTETLDDQDSPDHQEKEVSIH
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F -> Q (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                    NONHELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENE CAUSE TEMPERATURE-SENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                        NHELICAL REGION (NC1).
1637 (BY SIMILARITY).
1640 (BY SIMILARITY).
                                                                                                                7083D9AF63E05D45 CRC64;
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0.44;
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RESULT 20
YRF2_CAEEL
ID YRF2_C
AC Q09578
AC Q09578
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DT Q1
     RESULT 21
CALH_HUMAN
ID 2799060
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Q09578;
Q1-NOV-1997
Q1-NOV-1997
Q1-NOV-1997
                                                                                                                                                                                                                       CA1H_HUMAN STANDARD; PRT; 1516 AA.

P39060; Q9Y608; Q9Y607; Q9UK38;

01-FEB-1995 (Rel. 31, Created)

01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

COLLAGEN ALPHA 1(XVIII) CHAIN PRECURSOR (CONTAINS: ENDOSTATIN).
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JUL-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).

-i- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
SEQUENCE FROM N.A.
MEDLINE-98164096; PubMed-9503365;
MEDLINE-98164096; PubMed-9503365;
                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PF01391; Collagen; 2.
Hypothetical protein; Cuticle; Connective tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditidae; Peloderinae; Caenorhabditis NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U21318; AAC46668.1; -. WormPep; K03H9.2; CE01996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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                                                                                                             NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; K03H9
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SIMILARITY: TO OTHER COLLAGENS. STRONG,
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9; Conservative
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87 116
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285 /
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Primates;
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Pred. No.
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                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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          Pihlajaniemi T.;
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And tumor growth, plays a critical role in the maintenance of retinal restructure and in neural tube closure.";

RI Hum, Mol. Genet. 9:2051-2058(2000).

C -!- FUNCTION: COLA18A PROBABLY PLAYS A MAJOR ROLE IN DETERMINING THE RETINAL STRUCTURE AS WELL AS IN THE CLOSURE OF THE NEURAL TUBE.

C -!- FUNCTION: ENDOSTATIN POTENTLY INHIBITS ENDOTHELIAL CELL PROLIFERATION AND ANGIOGENESIS. MAY INHIBIT ANGIOGENESIS BY BINDING TO THE HEPARAN SULPHATE PROTEOGLYCANS INVOLVED IN GROWTH FACTOR SIGNALLING (BY SIMILARITY).

C -!- TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS FORM/NC-493 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

C -!- TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS IN LIVER, LUNG AND KIDNEY.

C -!- TISSUE SPECIFICITY: PRESENT IN MULTIPLE ORGANS WITH HIGHEST LEVELS OF THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HUDROXILATED IN SOME OR ALL OF THE CHAINS AND AND AND SECRETIVAL DESCREATION WITH RETINAL DESCREATE OF KNOBLOCH SYNDROME (KS);

C -!- DISEASE: DEFECTS IN COL18A1 ARE A CAUSE OF KNOBLOCH SYNDROME (KS);

C -!- SIMILARITY: BELONGS TO THE MULTIPLE ENCEPHALOCELE.

C -!- SIMILARITY: BELONGS TO THE MULTIPLE ENCEPHALOCELE.
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RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Merchwald K., Rump A., Schillabbel M., Schudy A., Zimmermann W.,
RA Reichwald K., Rump A., Schillabbel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Minoshima S., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
RN Nature 405:311-319(2000).
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Genomics 19:494-499(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Passos-Bueno M.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INVOLVEMENT IN KNOBLOCH SYNDROME
                                                                                                                                                                    ween the Swiss Institute of Bioinfi
European Bioinformatics Institute.
                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                  non-profit institutions as long as its content and this statement is not removed. Usage by an
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cell adhesion; Collagen; Glycoprotein; Signal; Alternative spli
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EMBL; AF184060; AAF01310.1;
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SHORT ISOFORM).
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Query Match Best Local S Matches 10

l Similarity 66. 10; Conservative

63.0%;

Score Pred. 1; Mis

58; D

DB 1; 0.54;

Length 1516

Indels

0

Gaps

0

Mismatches

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517

|:|| || || || | GLKGQKGEPGVPGPP 531

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RESULT 22
CA24_CAEEL
EMBL; Z22964;
EMBL; Z22964;
EMBL; J05066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P17140;
01-AUG-1990 (Rel. 15, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-94012964; PubMed-7691828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sibley M.H., Graham P.L., von Mende N., Kramer J.M.; "Mutations in the alpha 2(IV) basement membrane collagen Caenorhabditis elegans produce phenotypes of differing se EMBO J. 13:3278-3285(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The two Caenorhabditis elegans basement membrane (type IV) collagen genes are located on séparate chromosomes.";
J. Biol. Chem. 264:17574-17582(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genetic identification, sequence, Caenorhabditis elegans alpha 2(IV)
J. Cell Biol. 123:255-264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LET-2 OR CLB-1.
Caenorhabditis elegans.
                                                                     or send
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guo X., Kramer J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
MEDLINE-90008929; PubMed-2793871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic identification, se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA24_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94320591; PubMed-8045258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 1495-1758 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: FORM I IS PREDOMINANT IN EMBRYOS AND FORM II IS PREDOMINANT IN THE LARVAE AND ADULTS.

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH ME CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 7S DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES. SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN. TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND BETWEEN NC1
                                                                                                                                                                                                                  DISEASE: MUTATIONS IN LET-2 ARE GENERALLY EMBRYONIC LETHAL.
                                                                                                                                                                                                                                                                     PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. PTM: TYPE IV COLLAGENS CONTAIN UNMERCUS CYSTEIRE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAINS.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; I (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODUCED BY ALTERNATIVE SPLICING.
                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        LOCATED IN
; CAA80536.1; -.
; CAA80537.1; -.
; AAA27989.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                        THE
                                                                                                                                                                                                                                                        NC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mello C.C., Kramer J.M.;
equence, and alternative splicing
                                                                                                                                                                                                                                                        DOMAIN, ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1758 AA
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ING. 12 OF
YOWN TYPE
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RESULT /23
CC34_CAEEL
ID CC34_CAEEL
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Best Local
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                                                                                                                                                                              01-FEB-1994
01-FEB-1994
01-JUN-1994
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DISULFID
DISULFID
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SEQUENCE
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VARIANT
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VARIANT
VARIANT
VARIANT
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"Sequence comparison of the Caenorhabditis elegans genes, and their deduced collagen products."; Gene 120:261-266(1992).
-I- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGEL PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOS
                                                                   SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-93013043; PubMed-1398138;
                                                                                                             Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01391; Collagen; 23.
Hydroxylation; Connective tissue; Basement membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001442; -. Pfam; PF01413; C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U22327; AAA64312.1;
PIR; A34476; A34476.
                                                          Bird D.M.;
                                                                                                                                               Caenorhabditis elegans
                                                                                                                                                          COL-34.
                                                                                                                                                                     CUTICLE COLLAGEN 34.
                                                                                                                                                                                                                P34687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                416 GPKGDKGDGGIPGAP 430
                                                                                                                                                                                                                                                                                                       1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                       Similarity
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877
904
1003
1125
1152
1286
1682
1758
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1546
1579
1591
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                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                             28, Created)
28, Last sequence up
29, Last annotation
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1527
1758
1635
1632
1632
1750
1750
1747
1777
1707
                                                                                                                                    Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                       63.0%;
                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                    167750
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                                                                                                                          Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                           G-> E (IN MN114; 73% LETHAL).
A-> T (IN MN126; 100% LETHAL).
G-> E (IN MN109; 37% LETHAL).
G-> R (IN MN109; 37% LETHAL).
G-> R (IN MN103 AND MN151; 96% LETHAL).
G-> R (IN MN101; 100% LETHAL).
G-> E (IN MN101; 100% LETHAL).
G-> E (IN MN101; 100% LETHAL).
G-> E (IN MN101; 100% LETHAL).
G-> R (IN G30; 90% LETHAL).
G-> R (IN G30; 90% LETHAL).
G-> R (IN G30; 90% LETHAL).
G-> D (IN G30; 90% LETHAL).
G-> D (IN G30; 90% LETHAL).
G-> D (IN MN109; 20% LETHAL).
G-> D (IN G25; 28 LETHAL).
G-> D (IN G37 AND B246; 9% LETHAL).
G-> D (IN G37 AND B246; 9% LETHAL).
D-> L (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
OR 1632 (BY SIMILARITY).
OR 1635 (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
OR 1747 (BY SIMILARITY).
OR 1750 (BY SIMILARITY).
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCA
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                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                       Score 58; DB 1;
Pred. No. 0.62;
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DIGAMGPAGPPGPIASTMSKGTIIGPKGDLGEKGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISOFORM II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    97EE3F3DBB2D2AC5 CRC64;
 COMPOSED LARGELY
BOTH AS AN EXOSKE
                                                                                                                                                                                           update)
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  AS AN EXOSKELETON AND
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                                                                                                                                                                                                                                                                                                                                                  Length 1758
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                                             dpy-13
             OF COLLAGEN-LIKE
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                                              and
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                                              col-34
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RESULT 24
CA13_MOUSE
ID CA13_MOUSE
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Best Local
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01-AUG-1988 (Rel. 08, Created)
15-JUL-1999 (Rel. 38, Last seg
01-OCT-2000 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                    Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and fi
                                                                                                                          Wood L., Therlault N., Vogeli G.; "Complete nucleotide sequence of the N-terminal domains of the murine alpha-1 type-III collagen chain."; Gene 61:225-230(1987).
                                                                                                                                                                                   SEQUENCE OF 1-488 FROM N.A. MEDLINE=8816,7858; Pubmed=3443309;
                                                                                                                                                                                                                                "The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA sequence.";
Gene 147:161-168(1994).
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL X DBA; TISSUE=Embryo;
MEDLINE=95011609; PubMed-7926795;
                                                                                                                                                                                                                                                                                                                                                                                                           COL3A1
                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Last sequence update) 01-0CT-2000 (Rel. 40, Last annotation updat COLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuticle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                         (III) collagen
                                                                                                                                                                                                                                                                            Toman D., de Crombrugghe B.;
                                                                                  MEDLINE=85131189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GPKGPKGPPGAPGAP 198
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                            Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GVKGDKGNPGWPGAP 15
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SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLLAGENS.
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얽
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                                                                                                 OF 1-28 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000087; -.
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151
181
215
298 /
1442-1464 FROM N.A
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                          gene.";
260:3773-3777(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                   PubMed=3972847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.0%;
73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW;
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TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57; DB Pred. No. 0.16 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                       first exon of the mouse alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on ong as its content is in no
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0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 298
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QΥ
RESULT 25
MSRE_MOUSE
                                                   В
                                                                                                                                                                                                       Matches
                                                                                                                Best
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52046; CAA36279.1; ...
EMBL; M18933; AAA37338.1; ...
EMBL; K3037; ...; NOT_ANNOTATED
EMBL; X57983; CAA41048.1; ...
PIR; A22287; A22287.
PIR; A27353; A27353.
PIR; S16373; S16373.
                                                                                                                                                                              DISULFID DISULFID
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                                                                                                                                                                                                                                                                                 DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                  Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                           PROPEP
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001007; -.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 17.
PROSITE; PS01208; VWFC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.";
Biochim. Biophys. Acta 1089:241-243(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:88453; Col3a1.
InterPro; IPR000087; -.
InterPro; IPR000885; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL;
MEDLINE=91274355; PubMed=2054384;
                                                   857
                                                                                                                Local
                                                                          1 GVKGDKGNPGWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALONG WITH TYPE I COLLAGEN.
SUBUNIT: TRIKERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
ALSO CROSS-LINKED VIA HYDROXYLYSINES.
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-LINKED GLYCAN CONSISTS OF GLC-GAL DISACCHARIDE (BY SIMILARITY). SIMILARITY: CONTAINS 1 VMFC DOMAIN.
                                                  GVKGERGSPGGPG
                                                                                                   Similarity 9; Conserv
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HYDROXYLÁTION (BY SIMILARITY).
                                                                                                                                                                    ₹.
                                                                                                                Pred. No.
                                                                                                                            Score 56;
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INTERCHAIN
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NONHELICAL REGION (N-TERMINAL).
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                CARBOXYL-TERMINAL PROPERTIDE
                                                                                                                                                                                                                                                                                                                                                          AMINO-TERMINAL PROPERTIDE. COLLAGEN ALPHA 1(III) CHAIN
                                                                                                                                                                                                                                                                                            NONHELICAL REGION (C-TERMINAL)
                                                                                                   Mismatches
                                                                                                                                                                    2104EC27A886090B CRC64;
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                                                                                                                             1;
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SIMILARITY).
                                                                                                                            Length 1464;
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MBL outstation -
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MSRE_MOUSE P30204;

STANDARD

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MEDLINE-93359822; PubMed-8394868; MEDLINE-93359822; PubMed-8394868;
                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                 J. LIPIG Res. 36:1305-1314(1995).

-I- FUNCTION: MEMBRANE GLYCOOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.
TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 349-458 FROM N.A.
MEDLINE-91062370; Pubmed-1978939;
Freeman M., Ashkenas J., Rees D.J., Kingsley D.M., Copeland N.G.,
Jenkins N.A., Krieger M.;
"An ancient, highly conserved family of cysteine-rich protein domains
"revealed by cloning type I and type II murine macrophage scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (SHORT FORM).

SEQUENCE FROM N.A. (SHORT FORM).

DOI T., Wadd Y., Kodama T., Higashi K.I., Kurihara Y.,

MIYAZAKI T., Nakamura H., Uesugi S., Imanishi T., Kawabe Y.,

Itakura H., Yazaki Y., Matsumoto A.;

"Charged collagen structure mediates the recognition of negatively

"Charged macromolecules by macrophage scavenger receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Lipid
[2]
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED LDL RECEPTOR I AND II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aftring R.P., Freeman M.W.;

"Structure of the murine macrophage scavenger receptor gene and evaluation of sequences that regulate expression in the macrophage evaluation of sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structures and high and low affinity ligand binding properties murine type I and type II macrophage scavenger receptors."; J. Lipid Res. 34:983-1000(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Euthers
NCBI_TaxID=10090;
               InterPro;
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                                                               L; L04274; AAA39747.1; ALT_INIT.

L; L04275; AAA39748.1; ALT_INIT.

L; D13382; BAA02650.1; -.

L; M59445; AAA37464.1; -.

L; M59446; AAA37465.1; -.

L; U13873; AAC13774.1; -.
                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                              ę
                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHAGE SCAVENGER
RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTERNATIVE SPLICING
                                   A38260; A38260.
MGI:98257; Scvr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               line, P388D.
                                                                                                                                                                                                                                                                                                                                              THE SAME GENE.
                                                                                                                                                                                               an email to license@isb-sib.ch).
IPR000087;
IPR001190;
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Rodentia;
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DOMAIN
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PROSITE; PS00420; SRCR_1; 1.
Transmembrane; Glycoprotein; Endocytosis; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heptad repeat pattern; Receptor; Alternative splicing.
DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
TRANSMEM 56 78 SIGNAL-ANCHOR (TYPE-II ME
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12; Conserv
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N-LINK
                                                                                                                               Score 55.5;
Pred. No. 0
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ALPHA-HELICAL COILED-COIL.
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                                                                                                                                                                                                                                          6D4C041C27EEE50B CRC64;
                                                                                                        Mismatches
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Search completed: May 23, 2001, 16:17:17 Job time: 83 sec

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Title:
Perfect score:
Sequence:
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 Q9VYY2
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                               O9vvy2 drosophila
Q16593 homo sapien
O90612 gallus gall
O92029 gallus gall
O9und9 homo sapien
O9ngk9 homo sapien
O02802 homo sapien
O18407 drosophila
Q9vmv5 drosophila
Q63870 mus musculu
Q26312 strongyloce
                                                                                                               Q14052 homo sapien
Q90585 gallus gall
Q919k3 gallus gall
Q14054 homo sapien
                                                                                       Q26054 paracentrot
Q26634 strongyloce
Q17163 brugia mala
                                                                                                                                                Q9nub7 homo sapien
                                                                                                                                                               Description
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Q9z1k4 rattus norv	Q9Z1K4	1	295		56	45
Q9uc14 homo sapien	Q9UC14	4	284	60.9	56	44
Q9nzq6 homo sapien	Q9NZQ6	4	1745		57	43
Q9jli2 mus musculu		11	1739		57	42
Q9qzs0 mus musculu		=	1669		57	41
Q60444 cricetulus		11	1549		57	40
Q9u9k7 caenorhabd1	ດ	G	1117		57	39
O93484 oncorhynchu		13	940		57	38
077087 alvinella p		S	890		57	37
		ű	778		57	36
P90679 arenicola m		Ⴠ	684		57	35
O17866 caenorhabd1	0	Ç,	650		57	34
Q9wub9 mesocricetu			483		57	ω G
Q9np19 homo sapien	o	4	446		57	32
P78429 homo sapien		4	132		57	31
Q19099 caenorhabdi		Ç	1759		58	30
Q19098 caenorhabd1		Ç,	1758		58	29
Q9y6q8 homo sapien		4	1516		58	28
Q9y6q7 homo sapien	o	4	1336		58	27
Q90412 brachydanio		13	464		58	26
O9jiO4 rattus norv		11	1737		59	25
Q9qzr9 mus musculu		11	1682	64.1	59	24
Q07563 mus musculu	Q07563	님	1433	64.1	59	23
Q9jmh4 mesocricetu	Q9JMH4	11	1431	64.1	59	22
Q9ujc7 homo sapien	Q9UJC7	4	771	64.1	59	21
Q07265 strongyloce	Q07265	v	1752	64.7	59.5	20

ALIGNMENTS

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RESULT Q14052 ID Q1 AC Q1 DT 01 DT 01 DT 01 DT 01 DT 01 DE AI GN CC OS HC
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Best Local Similarity 73.3
Matches 11; Conservative
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Q9NUB7;
Q9NUB7;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2000
            014052 PRELIMINARY; PRT; 673 AA. 014052; PREMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) ALPHA-2 TYPE IV COLLAGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                   Collagen.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              A24...
COL4A5.
Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata;
Tharvota; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
02-24-33.1 (COLLAGEN, TYPE IV, ALPHA 5 (ALPORT SYNDROME)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL035425; CAB90289.1; -.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                   Cobley V
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                             |:||:||||| || || 480 GIKGEKGNPGQPGLP
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                                                                                                                                                                                                                                                                                    886 AA; 85478 MW;
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                                                                                                                                                                                                                              75.0%;
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                                                                                                                                                                                                                Score 69; DB 4;
Pred. No. 0.023;
2; Mismatches
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Chordata;

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MEDLINE=90062114; PubMed=2584206;

Nishimura I., Muragaki Y., Olsen B.R.;

"Tissue-specific forms of type IX collagen-proteoglycan use of two widely separated promoters.";

J. Biol. Chem. 264:20033-20041(1989).

EMBL; M28660; AAA48709.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CARTILAGE ALPHA-1(IX) COLLAGEN-PROTEOGLYCAN (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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EMBL; M24766; AAA52043.1; -
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Mammalia; Eutheria;
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MEDLINE=94012661;
Hoffman G.G., Lee
                                                  TISSUE-PLACENTA;
                                                                    SEQUENCE FROM N.A.
                                                                                                             "The carboxyl-terminal half of type VII collagen, including collagenous NC-2 domain and intron/exon organization of the corresponding region of the COL7Al gene."; Hum. Mol. Genet. 2:273-278(1993).
                                                                                                                                                                                                    MEDLINE=93271985; PubMed=8499916; Greenspan D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.";
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Parente M.G., Chung L.C., Ryynanen J., Woodley D.T., Wynn K.W.,
Bauer E.A., Mattel M.G., Chu M.L., Uitto J.;
"Human type VII collagen: cDNA cloning and chromosomal mapping
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DOLTAI.

Homo sapiens (Human).

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Gallus gallus (Chicken).
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    Chung-Honet
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0.21;
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      L.C.,
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    Cheng
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RESULT
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Best Local Similarity
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Best Local Similarity
Matches 12; Conserv
     Matches
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HSSP; P12111; IKNT.
INTERPRO; IPRO00087; -
INTERPRO; IPR001777; -
INTERPRO; IPR002035; -
INTERPRO; IPR002223; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PFUVUJ.; COllagen; Z...
PFAM; PF01391; COllagen; Z...
PRINTS; PR00453; VWFADOMAIN.
PRINTS; PR00759; BASICPTASE.
PROSTTE; PS00280; BPTI_KUNITZ; 1.
PROSTTE; PS00280; BPTI_KUNITZ; 1.
POTENTIAL.
23 COLLAGEN TYPE VII.
PARSEE640D4C39545 CRCf
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-89149773; PubMed-2537631;
Saitta B., Buttice G., Gambino R.;
Saitta B., Buttice G., Gambino R.;

"Isolation of a putative collagen-like Paracentrotus lividus.";
Biochem. Biophys. Res. Commun. 158:633-EMBL; M24558; AAA29439.1; ".
                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2354
                                                                                                                                                                                                                                                                                                                           COLLAGEN-LIKE (FRAGMENT)
Paracentrotus lividus (Common sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural organization of the human type VII collagen gene (Composed of more exons than any previously characterized gene.", Genomics 21:169-179(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christiano A.M., Hoffman G.G., Chung-Honet L.C., Uitto J., Greenspan D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location of the gene for the cytochrome c reductase.";
                                                                                                                     INTERPRO; IPRO00087; -. PFAM; PF01391; Collagen; 4.
                                                                                                                                                                                                                                                                                                               Paracentrotus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q26054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q26054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-87 FROM
                                                                                                                                                                                                                                                                                           NCBI_TaxID-7656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katchman S., Uitto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVKGDKGNPGWPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVKGDLGLPGLPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00014; Kunitz_BPTI;
PF00041; fn3; 9.
PF00092; vwa; 2.
PF01391; Collagen; 21.
                                                                                      290 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268:21113-21119(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J., Greenspan D.S.;
requence, intron/exon organization,
                                                                                      26174 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                     67.48;
78.68;
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Last annotation updat
     μ,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                     Score 62; DB 5;
Pred. No. 0.083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 63; I
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                        158:633-639(1989).
                                                                                      FA221A1BF1E67D2F CRC64;
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290
                                                                                                                                                                                                          gene
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0.64;
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     Indels
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RESULT

Q26634

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ID 620

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AC Q2
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Best Local S
Matches 11
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01-NOV-1996
01-NOV-1996
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01-NOV-1996 (Trem
01-JUN-2000 (Trem
ALPHA-1 COLLAGEN.
                               "The structural organization of an alpha 2 collagen gene from the filarial nematode B Mol. Blochem. Parasitol. 70:227-229(1995). EMBL; U07224; AAC46611.1; -. INTERPRO; IPRO00087; -. INTERPRO; IPRO01442; -. PFAM; PF01331; Collagen; 23. PFAM; PF01413; C4; 2.
                                                                                                                                                                               STRAIN-APERIODIC;
MEDLINE-95364846; PubMed-7637709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF01391; Collagen; PFAM; PF01410; COLFI; 1. PRODOM; PD002078; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2(I) collagen.";
J. Biol. Chem. 267:15559-15562(1992).
EMBL; M92040; AAA30035.1; -.
                                                                                                                                                                      Caulagi V.R., Rajan T.V.;
                                                                                                                                                                                                                                                        Onchocercidae; ENCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                             Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                              Q17163
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NCBI_TaxID=7668;
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           A2 (IV) BASEMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLP1ALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sea urchin collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 GSKGDQGNPGQPGA
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11; Conserv
                   PD003923;
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5 (TrEMBLrel.
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     1802
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(TremBLrel. 01, Last sequence up
(TremBLrel. 14, Last annotation
ement membrane Collagen (IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                         Brugia.
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78.6%;
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     172402
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01,
   MW.
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     595F16554CBE2D24 CRC64;
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IV) basement membrane nalay1.";

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Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
Echinoidea; Euechinoidea; Echinacea; Echinoida; S
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                            Solursh M.,
                                                                  .94D9CDA71A9FD73D CRC64;
                                                                                                                                                                                                                                                                                      homologous to vertebrate
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                                                                                                                                                                                                                                                                                                            Ramirez F.;
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Length 1414;
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RESULT
Q9VVY2
        ACD CONTROL OF THE CO
                                                                                                                               RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Mamantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pranakoch C., Baldwin D.,
Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangellsta C.C., Ferraz C., Ferriera S., Pleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harli N.K. Alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harli N.K. Alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harli N.K. Alush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Mount S.M., Moyn M., Murphy E., Muzny D.M., Nelson D.L.,
RA Lie W., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moyn M., Murphy E., Muzny D.M., Nelson D.L.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Wang A.H., Wang X.,
RA Spier E., Stapleton M., Strong G., Zhao Q., A.,
Ra Mang Z.-Y. Nassaman D.A., Meinstock 
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Best Local Similarity
Matches 10; Conserv
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01-MAY-2000
01-JUN-2000
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VVY2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Н
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                                                              PF01391; Collagen; 1
                                   PR01217;
                                                                                         IPR002965;
                                                                                                             IPR000087; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster (Fruit 1
Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophilidae; Drosophila.
PRICHEXTENSN.
A; 24308 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1209
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71.4%;
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13, Last sequence 14, Last annotations
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Pred.
F84B9C912D8EC1CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly).
; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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annotation update)
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SEQUENCE
  EMBL;
                 Nah H.D., Niu Z., Adams S.L.;
"An alternative transcript of the chick type does not encode type III collagen.",
J. Biol. Chem. 269:16443-16448(1994).
                       J. Biol
                                                                                                                                                                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
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01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-CCT-2000 (TIEMBLIEL 15, Last annotation update)
CCLLAGEN-LIKE PROTEIN (447 AA) (FRAGMENT).
                                                                                                   MEDLINE=94266842; PubMed=8206952;
                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                            HYPOTHET ICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X14963; CAA33085.1; -. EMBL; X15038; CAA33142.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           SEQUENCE
                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PLACENTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=PLACENTA;
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  U07974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01391; Collagen; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 14, Last annotation updata)
L PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑA;
                                                                                                                                                                                                          Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
41829 MW;
                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
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73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                            Galliformes;
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                                                                                                                                                                                                                                                                                                                                                                                                  310
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                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                                                                                                                                                                            Phasianidae;
                                                                                                                                                                                                                                                                                                                update)
                                                              III collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 224;
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                                                                                                                                                                                                            Phasianinae;
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Matches 10
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
180 KDA BULLOUS PEMPHIGOID ANTIGEN 2/TYPE XVII COLLAGEN
BPAG2/COL17A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94266842; PubMed-8206952;
Nah H.D., Niu Z., Adams S.L.;
Nah H.D., niu Z., Adams S.L.;
"An alternative transcript of the chick type III collagen gene that does not encode type III collagen.";
J. Biol. Chem. 269:16443-16448(1994).
EMBL; U07973; AAA83407.1; -.
INTERPRO; IPRO001007; -.
INTERPRO; IPRO01007; -.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ALPHA-1 COLLAGEN TYPE III (FRAGMENT).
SEQUENCE FROM N.A. MEDLINE-97164601; PubMed-9012408;
                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
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                                                                                                                                           Homo sapiens
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                                                                        NCBI_TaxID-9606;
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PF01391; Collagen;
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a; Aves; Neognathae; Galliformes; Phasianidae;
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310 AA; 27601 MW;
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                                                                                                                                         (Human)
                                                                                           Chordata;
Primates;
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71.4%;
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Pred. No. 0.18;
                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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"Cloning of the I
of novel mutation
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Am. J. Hum.
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076568 AAB51499.1

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076570 AAB51499.1

076571 AAB51499.1

076572 AAB51499.1

076573 AAB51499.1

076574 AAB51499.1

076575 AAB51499.1

076576 AAB51499.1

076577 AAB51499.1

076578 AAB51499.1

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0765881 AAB51499.1

0765882 AAB51499.1

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(COLLAGEN, TYPE XVII, ALPHA 1 (BP180)).
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                          Eukaryota; Metazoa; Arthropoda; Trache; Pterygota; Neoptera; Endopterygota; Di Ephydroidea; Drosophilidae; Drosophila; NCBI_TaxID-7227;
                                                                                COLLAGEN TYPE
                                                                                        01-JAN-1998
01-JUN-2000
                                                                                                                   018407;
                                                                                                                                                                                                                                                              PFAM; P
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AL138761; CAC00589.1; -.
Collagen.
SEQUENCE 1497 AA; 150418 MW; E01027005F3AE
 Yasothornsrikul
                                                    Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tra
                                                                                                          01-JAN-1998
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                                                                       DMCOLA2
                                                                                                                                                                                                                                                                                                    MEDLINE=92381323; PubMed=1324962; Giudice G.J., Emery D.J., Diaz L.A.; "Cloning and primary structural analysis autoantigen BP180.";
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; M91669; AAA35605.1;
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11; Conservative
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Primates;
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Kimbrell D.A.
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                                            Brachycera; Muscomorpha;
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Goorg F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., McPherson D.,

RA Markillov G. Milshina N.V., Mocharry C., McLeed M.P., McPherson D.,

RA Markillov G. Milshina N.V., Mocharry C., McLeed M.P., McPherson D.,
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Matches 10
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.N., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese Palazzolo M., Pittman G.S., Saunders R.D.C., Scheeler F., Shen H. Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spler E., Spradling A.C., Stapleton M., Strong R., Sun E., Syler E., Spradling A.C., Stapleton M., Strong R., Sun E., Syler E., Tector C., Turner R., Venter E., Wang A.H., Wang X. Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z., Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheo
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Q9VMV5;
01-MAY-2000
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A
George R.A., Lewis S.E., Richards S., Ashburner M.,
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01-JUN-2000
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Eukaryota; Metazoa; Arthropoda; Tracheata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006;
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175955 MW;
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., Galle R.F.,
Henderson S.N.,
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                                                                                                                       Shen H.,
                                                            Wang X.,
                                                                                                                                          Reese M.G.,
  o Q.A.,
Zheng
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RL Science 287:2185-2195(2000).
REMBL; AE003608; AAF52203.1; -.
FELYBASE; FEBNO016075; vkg.
R INTERPRO; IPR000087; -.
1 PFAM; PF01391; Colling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Ma
Best Loc
Matches
                    INTERPRO: IPRO02035; -.
INTERPRO: IPRO02223; -.
PFAM: PF00014; Kunitz_BPTI; 1.
PFAM: PF00041; fn3; 9.
PFAM: PF00092; vwa; 2.
PFAM: PF01391; Collagen; 22.
PFAM: PF00159; WFADOMAIN.
PRINTS: PR00453; VWFADOMAIN.
PRINTS: PR00759; BASICPTASE.
PROSITE: PS00280; BPTI_KUNITZ; 1
                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KIVÍTÍKKO S., LÍ K., Christ
SUDMÍLTED (JUL-1995) to the
EMBL; U32107; AAB65593.1; -
EMBL; S63654; AAB27492.1; -
HSSP; P12111 2KNT.

MGD; MGI:88462; Col7a1.

INTERPRO; IPRO00087; -
INTERPRO; IPRO01777; -
INTERPRO; IPRO01777; -
INTERPRO; IPRO02035; -
INTERPRO; IPRO02035; -
INTERPRO; IPRO02035; -
INTERPRO; IPRO02035; -
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-93315168; PubMed-8325648;

L1 K., Christiano A.M., Copeland N.G., Gilbert D.J., Chu M.L.,

L1 K., Christiano A.M., Copeland N.G., Gilbert D.J., Chu M.L.,

Jenkins N.A., Uitto J.;

"cDNA cloning and chromosomal mapping of the mouse type VII collagen

"cDNA cloning and chromosomal mapping of the mouse type VII collagen

"cDNA cloning and chromosomal mapping of the mouse type VII collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Mus musculus (Mouse).
**Trota; Metazoa; Chordata;
**Trota; Rodentia;
                                                                                                                                                                                                                                                                  Kivirko S., Li K., Christiano A.M., Uitto J.;
"Cloning of mouse type VII collagen reveals evolutionary
of functional protein domains and genomic organization.";
J. Invest. Dermatol. 106:1300-1306(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
SEQUENCE
                                                                                                                                                                                                                                                                                                                     MEDLINE-96275720; PubMed-8752674;
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PF01413; C4; 2.
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295116 MW;
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596FA507BC6C02C2 CRC64;
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Matches 11
                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=93186842; PubMed=8444899;
Exposito J.Y., D'Alessio M., Di Liberto M.

"Complete primary structure of a sea urchi
chain and analysis of the 5' end of its ge
J. Biol. Chem. 268:5249-5254(1993).

EMBL; L02917; AAA30039.1; -.

INTERPRO; IPR001442; -.
                                                                                                                                                                                                                                   Q07265;
Q07265;
Q1-NOV-1996
Q1-NOV-1996
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Q26312;
                                                                                                                                                                          Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wessel G.M., Etkin M., Benson S.;
"Primary mesenchyme cells of the sea
autonomously produced, nonfibrillar o
Dev. Biol. 148:261-272(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2377
         PFAM; PF01391; Collagen; PFAM; PF01413; C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92038439; PubMed=1936564;
Wessel G.M., Etkin M., Benson S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
NONFIBRILLAR COLLAGEN (FRAGMENT).
                                                                                                                                                                 Strongylocentrotus.
                                                                                                                                                                                                              COLP3ALPHA.
                                                                                                                                                                                                                          PROCOLLAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus.
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                                                                                                                                                    NCBI_TaxID-7668,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S64572; AAB20270.1; -. PRO; IPRO00087; -. PF01391; Collagen; 13.
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                         ALPHA 1(III)
                                                                                                                                                                                                                                 (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Pred. No.
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Pred. No. 0.
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                                                                                           Liberto M., Ramirez
a sea urchin type IV
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collagen for spiculogenesis.";
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Matches 13
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Best Local Similarity
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COL4A5 (COLL
COL4A5.
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NON_TER
SEQUENCE
                                                                                                                                                       "Yamamoto K., Inoue N., Fujimori A., Saito T.,
"Mesocricetus auratus mRNA for type XVII coll
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ
EMBL; AB027759; BAA94381.1; -.
SEQUENCE 1431 AA; 144579 MW; 4315631FEB2CS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrembLrel.
01-OCT-2000 (TrembLrel.
01-OCT-2000 (TrembLrel.
COLLAGEN TYPE XVII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Rodentia; Sciurogn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ЈМН4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus
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-2000 (TIEMBLIFE1. 13, Last Sequence update)
-2000 (TIEMBLIFE1. 14, Last annotation update)
(COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR) (FRAG
      10;
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: 72760 MW;
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Score 59; DB
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2; Mismatches
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Pred. No. 1
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Sciurognathi;
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                                                                                                                                                                                                                                                        Saito T., Shinkai H., XVII collagen.";
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thi; Muridae; Cricetinae;
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Q07563
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                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
                                                                                                                                    Q9QZR9 PRELIMINARY;
Q9QZR9;
Q1-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-OCT-2000 (TrEMBLrel. 15, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li K., Tamai K., Tan E.M., Uitto J.;

"Cloning of type XVII collagen. Complementary and genomic DNA sequences of mouse 180-kilodalton bullous pemphigoid antigen (BPAG2) predict an interrupted collagenous domain, a transmembrane segment, and unusual features in the 5'-end of the gene and the 3'-untranslated region of the mRNA.";

J. Biol. Chem. 268:8825-8834(1993).
-i- FUNCTION: THE COLLAGEN DOMAINS OF BP180 ALLOW THE HEMIDESMOSOME TO FORM STABLE INVERACTIONS WIH THE CONSTITUENTS OF THE EXTRACELLULAR MATRIX OF THE CUTANEOUS BASENENT MEMBRANE ZONE.

-i- SUBCELLULAR LOCATION: A COMPONENT OF THE HEMIDESMOSOME.
-i- SUBCELLULAR LOCATION: A COMPONENT OF THE HEMIDESMOSOME.
-i- DISEASE: UPON DISRUPTION OF BP180 BY AUTOANTHODIES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q07563;
Q07563;
Q1-NOV-1996
Q1-NOV-1996
                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MEDLINE=20005934; Public W., Phillips C.L.,
                         SEQUENCE FROM N.A.
TISSUE-KIDNEY;
                                                              NCBI_TaxID=10090;
                                                                                                      Mus musculus (Mouse).
                                                                                                                    COL4A4.
                                                                                                                                ALPHA 4 COLLAGEN IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BULLOUS PEMPHIGOID (BP).
EMBL; L08407; AAA37443.1; -.
MGD; MGI:88450; CO117a1.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO00087; -. PFAM; PF01391; Collagen; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93232041; PubMed=8473327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                               Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                               948 GPKGDQGDPGVPGTP
                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                         1 GVKGDKGNPGWPGAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMIDESMOSOME IS DISRUPTED LEADING TO THE BLISTERING SKIN DISORDER
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                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                               Cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                  1433 AA;
                                                                                                                                                                                                                                                                                                                   Conservative
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PubMed=10534397;
.L., Killen P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
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66.78;
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01,
14,
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14, Last annotation update)
ALPHA 1 (BULLOUS PEMPHIGOID
                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                               Score 59;
Pred. No.
                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
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Hlaing
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                                                                              Muridae;
 Harrison
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RESULT 25
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Search completed: May 23, 2001, 16:17:05 Job time: 96 sec
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                 Query Match 64.1%;
Best Local Similarity 76.9%;
Matches 10; Conservative
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elder F.F.B., Miner J.H., Overbeek P.A., Meisler M.H.;
"Insertional mutation of the collagen genes col4a3 and col4a4 in a mouse model of alport syndrome.";
Genomics 61:113-124(1999).
EMBL; AF1693B8; AAD50450.1;
EMBL; AF1693B8; AAD50450.1;
INTERPRO; IPRO00087; -.
INTERPRO; IPRO01442; -.
PFAM; PF01413; C4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JI04;
                                                                                                                                                                                                         4 chain.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272661; AAF76432.1;
COllagen.
SEQUENCE 1737 AA; 171574 MW; D635D5D57481C257 CRC64;
                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ALPHA 4 TYPE V COLLACEN.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                              STRAIN-SPRAGUE DAWLEY;
Chernousov M.A., Rothblum K.N., Tyler W.A., Stahl R.C., Carey D.J.;
"Schwann cells synthesize type V collagen that contains a novel alpha
                                                                       1 GVKGDKGNPGWPG 13
| |||:|||| ||
| 740 GPKGDRGNPGLPG 752
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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|::||:||:|| || 1
176 GIQGDRGDPGPPGLP 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.1%;
                                                                                                                                Score 59; DB 1
Pred. No. 1.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1737 AA
                                                                                                                                                                                                            D635D5D57481C257 CRC64;
                                                                                                                                                             DB 11; Length 1737;
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